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| (54) Title: NOVEL COMPOUNDS | | | |
| (57) Abstract <p>This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy.</p> | | | |

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NOVEL COMPOUNDS

Field of the Invention:

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the
5 production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy. Preferred embodiments of the invention include Streptococcal polypeptides and polynucleotides, particularly those of *Streptococcus pneumoniae*.

10 Background of the Invention:

The Streptococci make up a medically important genera of microbes known to cause several types of disease in humans, including otitis media, pneumonia and meningitis. Since its isolation more than 100 years ago, *Streptococcus pneumoniae* has been one of the more intensively studied microbes. For example, much of our early understanding that
15 DNA is, in fact, the genetic material was predicated on the work of Griffith and of Avery, Macleod and McCarty using this microbe. Despite the vast amount of research with *S. pneumoniae*, many questions concerning the virulence of this microbe remain.

While certain Streptococcal factors associated with pathogenicity have been identified, e.g., capsule polysaccharides, peptidoglycans, pneumolysins, PspA Complement
20 factor H binding component, autolysin, neuraminidase, peptide permeases, hydrogen peroxide, IgA1 protease, the list is certainly not complete. Further very little is known concerning the temporal expression of such genes during infection and disease progression in a mammalian host. Discovering the sets of genes the bacterium is likely to be expressing at the different stages of infection, particularly when an infection is established, provides
25 critical information for the screening and characterization of novel antibacterials which can interrupt pathogenesis. In addition to providing a fuller understanding of known proteins, such an approach will identify previously unrecognised targets.

Brief Description of the Invention:

This invention provides novel proteins, particularly those from *Streptococcus*
30 *pneumoniae*, strain 0100993, characterised in that it comprises the amino acid sequences given herein or fragments, analogues or derivatives thereof.

In accordance with another aspect of the present invention, there are provided polynucleotides (DNA or RNA) which encode such polypeptides.

In particular the invention provides polynucleotides having the DNA sequences given herein.

The invention also relates to novel oligonucleotides derived from the sequences given herein which can act as PCR primers in the process herein described to determine whether or not the *Streptococcus pneumoniae* gene identified herein in whole or in part is expressed in infected tissue. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. The proteins so identified are also useful as targets in screens designed to identify antimicrobial compounds.

It is an object of the invention to provide polypeptides that have been identified as novel polypeptides by homology between the amino acid sequence set out in the Sequence Listing and a known amino acid sequence or sequences of other proteins such as the proteins identified under the heading Identity in Table 1.

It is a further object of the invention to provide polynucleotides that encode polypeptides set forth in the Sequence Listing, particularly polynucleotides that encode the polypeptide set forth in the Sequence Listing.

In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding polypeptides comprising the sequence set out in the Sequence Listing, or a variant thereof.

In another particularly preferred embodiment of the invention there is a novel protein from comprising an amino acid sequence of the Sequence Listing, or a variant thereof.

In accordance with another aspect of the invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization. Among the particularly preferred embodiments of the invention are naturally occurring allelic variants the polynucleotides set forth in the Sequence Listing and polypeptides encoded thereby.

In accordance with yet another aspect of the invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents, including, for example, antibodies.

In accordance with certain preferred embodiments of the invention, there are provided products, compositions and methods for assessing expression of the sequences the Sequence Listing, treating disease, for example, otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid, assaying genetic variation, and

administering a polypeptide or polynucleotide of the invention to an organism to raise an immunological response against a bacteria, especially a *Streptococcus pneumoniae* bacteria.

In accordance with certain preferred embodiments of this and other aspects of the invention there are provided polynucleotides that hybridize to polynucleotide sequences of the invention, particularly under stringent conditions.

In certain preferred embodiments of the invention there are provided antibodies against polypeptides of the invention.

In other embodiments of the invention there are provided methods for identifying compounds which bind to or otherwise interact with and inhibit or activate an activity of a polypeptide or polynucleotide of the invention comprising: contacting a polypeptide or polynucleotide of the invention with a compound to be screened under conditions to permit binding to or other interaction between the compound and the polypeptide or polynucleotide to assess the binding to or other interaction with the compound, such binding or interaction being associated with a second component capable of providing a detectable signal in response to the binding or interaction of the polypeptide or polynucleotide with the compound; and determining whether the compound binds to or otherwise interacts with and activates or inhibits an activity of the polypeptide or polynucleotide by detecting the presence or absence of a signal generated from the binding or interaction of the compound with the polypeptide or polynucleotide.

In accordance with yet another aspect of the invention, there are provided agonists and antagonists of the polynucleotide and/or polypeptides of the invention, preferably bacteriostatic or bacteriocidal agonists and antagonists.

In a further aspect of the invention there are provided compositions comprising a polynucleotide or a polypeptide of the invention for administration to a cell or to a multicellular organism.

Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

Detailed Description of the Invention:

Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. Because each of the sequences contains an open reading frame (ORF) with appropriate initiation and termination codons, the encoded protein upon expression can be used as a target for the screening of antimicrobial drugs. Additionally, the DNA sequences encoding preferably the amino terminal regions of the encoded protein or the Shine-Delgarno region can be used to construct antisense sequences

to control the expression of the coding sequence of interest. Furthermore, many of the sequences disclosed herein also provide regions upstream and downstream from the encoding sequence. These sequences are useful as a source of regulatory elements for the control of bacterial gene expression. Such sequences are conveniently isolated by
5 restriction enzyme action or synthesized chemically and introduced, for example, into promoter identification strains. These strains contain a reporter structural gene sequence located downstream from a restriction site such that if an active promoter is inserted, the reporter gene will be expressed.

Although each of the sequences may be employed as described above, this
10 invention also provides several means for identifying particularly useful target genes. The first of these approaches entails searching appropriate databases for sequence matches in related organisms. Thus, if a homologue exists, the Streptococcal-like form of this gene would likely play an analogous role. For example, a Streptococcal protein identified as homologous to a cell surface protein in another organism would be useful as a vaccine
15 candidate. To the extent such homologies have been identified for the sequences disclosed herein they are reported along with the encoding sequence.

Recently techniques have become available to evaluate temporal gene expression in bacteria, particularly as it applies to viability under laboratory and infection conditions. A number of methods can be used to identify genes which are essential to survival *per se*, or
20 essential to the establishment/maintenance of an infection. Identification of an ORF unknown by one of these methods yields additional information about its function and permits the selection of such an ORF for further development as a screening target. Briefly, these approaches include:

1) Signature Tagged Mutagenesis (STM)

25 This technique is described by Hensel *et al.*, *Science* 269: 400-403(1995), the contents of which is incorporated by reference for background purposes. Signature tagged mutagenesis identifies genes necessary for the establishment/maintenance of infection in a given infection model.

The basis of the technique is the random mutagenesis of target organism by various
30 means (e.g., transposons) such that unique DNA sequence tags are inserted in close proximity to the site of mutation. The tags from a mixed population of bacterial mutants and bacteria recovered from an infected hosts are detected by amplification, radiolabeling and hybridisation analysis. Mutants attenuated in virulence are revealed by absence of the tag from the pool of bacteria recovered from infected hosts.

In Streptococcus pneumoniae, because the transposon system is less well developed, a more efficient way of creating the tagged mutants is to use the insertion-duplication mutagenesis technique as described by Morrison et al., J. Bacteriol. 159:870 (1984) the contents of which is incorporated by reference for background purposes.

5 **2) In Vivo Expression Technology (IVET)**

This technique is described by Camilli et al., Proc. Nat'l. Acad. Sci. USA. 91:2634-2638 (1994), the contents of which is incorporated by reference for background purposes.

IVET identifies genes up-regulated during infection when compared to laboratory cultivation, implying an important role in infection. ORF identified by this technique are
10 implied to have a significant role in infection establishment/maintenance.

In this technique random chromosomal fragments of target organism are cloned upstream of a promoter-less recombinase gene in a plasmid vector. This construct is introduced into the target organism which carries an antibiotic resistance gene flanked by
15 resolvase sites. Growth in the presence of the antibiotic removes from the population those fragments cloned into the plasmid vector capable of supporting transcription of the recombinase gene and therefore have caused loss of antibiotic resistance. The resistant pool is introduced into a host and at various times after infection bacteria may be recovered and
20 assessed for the presence of antibiotic resistance. The chromosomal fragment carried by each antibiotic sensitive bacterium should carry a promoter or portion of a gene normally upregulated during infection. Sequencing upstream of the recombinase gene allows
25 identification of the up regulated gene.

3) Differential display

This technique is described by Chuang et al., J. Bacteriol. 175:2026-2036 (1993), the contents of which is incorporated by reference for background purposes. This method
25 identifies those genes which are expressed in an organism by identifying mRNA present using randomly-primed RT-PCR. By comparing pre-infection and post infection profiles, genes up and down regulated during infection can be identified and the RT-PCR product sequenced and matched to ORF 'unknowns'.

4) Generation of conditional lethal mutants by transposon mutagenesis.

This technique, described by de Lorenzo, V. *et al.*, Gene 123:17-24 (1993); Neuwald, A. F. *et al.*, Gene 125: 69-73(1993); and Takiff, H. E. *et al.*, J. Bacteriol. 174:1544-1553(1992), the contents of which is incorporated by reference for

5 background purposes, identifies genes whose expression are essential for cell viability.

In this technique transposons carrying controllable promoters, which provide transcription outward from the transposon in one or both directions, are generated. Random insertion of these transposons into target organisms and subsequent isolation of insertion mutants in the presence of inducer of promoter activity ensures that insertions which

10 separate promoter from coding region of a gene whose expression is essential for cell viability will be recovered. Subsequent replica plating in the absence of inducer identifies such insertions, since they fail to survive. Sequencing of the flanking regions of the transposon allows identification of site of insertion and identification of the gene disrupted. Close monitoring of the changes in cellular processes/morphology during growth in the

15 absence of inducer yields information on likely function of the gene. Such monitoring could include flow cytometry (cell division, lysis, redox potential, DNA replication), incorporation of radiochemically labeled precursors into DNA, RNA, protein, lipid, peptidoglycan, monitoring reporter enzyme gene fusions which respond to known cellular stresses.

20 5) Generation of conditional lethal mutants by chemical mutagenesis.

This technique is described by Beckwith, J., Methods in Enzymology 204: 3-18(1991), the contents of which are incorporated herein by reference for background purposes. In this technique random chemical mutagenesis of target organism, growth at temperature other than physiological temperature (permissive temperature) and subsequent

25 replica plating and growth at different temperature (e.g. 42°C to identify ts, 25°C to identify cs) are used to identify those isolates which now fail to grow (conditional mutants). As above close monitoring of the changes upon growth at the non-permissive temperature yields information on the function of the mutated gene. Complementation of conditional lethal mutation by library from target organism and sequencing of complementing gene

30 allows matching with unknown ORF.

6) RT-PCR

Streptococcus pneumoniae messenger RNA is isolated from bacterial infected tissue e.g. 48 hour murine lung infections, and the amount of each mRNA species assessed by reverse transcription of the RNA sample primed with random hexanucleotides followed by PCR

with gene specific primer pairs. The determination of the presence and amount of a particular mRNA species by quantification of the resultant PCR product provides information on the bacterial genes which are transcribed in the infected tissue. Analysis of gene transcription can be carried out at different times of infection to gain a detailed knowledge of gene regulation in bacterial pathogenesis allowing for a clearer understanding of which gene products represent targets for screens for novel antibacterials. Because of the gene specific nature of the PCR primers employed it should be understood that the bacterial mRNA preparation need not be free of mammalian RNA. This allows the investigator to carry out a simple and quick RNA preparation from infected tissue to obtain bacterial mRNA species which are very short lived in the bacterium (in the order of 2 minute halflives). Optimally the bacterial mRNA is prepared from infected murine lung tissue by mechanical disruption in the presence of TRIzol (GIBCO-BRL) for very short periods of time, subsequent processing according to the manufacturers of TRIzol reagent and DNAase treatment to remove contaminating DNA. Preferably the process is optimised by finding those conditions which give a maximum amount of *S.pneumoniae* 16S ribosomal RNA as detected by probing Northern blots with a suitably labelled sequence specific oligonucleotide probe. Typically a 5' dye labelled primer is used in each PCR primer pair in a PCR reaction which is terminated optimally between 8 and 25 cycles. The PCR products are separated on 6% polyacrylamide gels with detection and quantification using GeneScanner (manufactured by ABI).

Each of these techniques may have advantages or disadvantage depending on the particular application. The skilled artisan would choose the approach that is the most relevant with the particular end use in mind. For example, some genes might be recognised as essential for infection but in reality are only necessary for the initiation of infection and so their products would represent relatively unattractive targets for antibacterials developed to cure established and chronic infections.

Use of the of these technologies when applied to the ORFs of the present invention enables identification of bacterial proteins expressed during infection, inhibitors of which would have utility in anti-bacterial therapy.

Streptococcus pneumoniae, strain 0100993 has been deposited at the National Collection of Industrial and Marine Bacteria Ltd (NCIMB), Aberdeen, Scotland under NCIMB number 40794 on 11 April 1996, and a *Streptococcus pneumoniae*, strain 0100993 DNA library in *E. coli* was similarly deposited on 17 April 1996 under NCIMB number 40800.

The nucleotide sequences disclosed herein can be obtained by synthetic chemical techniques known in the art or can be obtained from *Streptococcus pneumoniae*, strain 0100993 by probing a DNA preparation with probes constructed from the particular sequences disclosed herein. Alternatively, oligonucleotides derived from a disclosed sequence can act as PCR primers in a process of PCR-based cloning of the sequence from a bacterial genomic source. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

To obtain the polynucleotide encoding the protein using the DNA sequence given herein typically a library of clones of chromosomal DNA of *Streptococcus pneumoniae*, strain 0100993 in *E. coli* or some other suitable host is probed with a radiolabelled oligonucleotide, preferably a 17mer or longer, derived from the partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using high stringency washes. By sequencing the individual clones thus identified with sequencing primers designed from the original sequence it is then possible to extend the sequence in both directions to determine the full gene sequence. Conveniently such sequencing is performed using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook, J. in MOLECULAR CLONING, A Laboratory Manual, 2nd edition, 1989, Cold Spring Harbor Laboratory (see: Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70).

A polynucleotide of the present invention may be in the form of RNA or in the form of DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequence which encodes the polypeptide may be identical to the coding sequence shown or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encoding the same polypeptide.

The present invention includes variants of the hereinabove described polynucleotides which encode fragments, analogues and derivatives of the polypeptide characterized by the deduced amino acid sequence given herein. The variant of the polynucleotide may be a naturally occurring allelic variant of the polynucleotide or a non-naturally occurring variant of the polynucleotide. In addition to the standard A, G, C, T/U representations for nucleic acid bases, the term "N" is also used. "N" means that any of the four DNA or RNA bases may appear at such a designated position in the DNA or RNA

sequence, except that N cannot be a base that when taken in combination with adjacent nucleotide positions, when read in the correct reading frame, would have the effect of generating a premature termination codon in such reading frame.

Thus, the present invention includes polynucleotides encoding the same
5 polypeptide characterized by the deduced amino acid sequence given herein as well as variants of such polynucleotides which variants encode for a fragment, derivative or analogue of the polypeptide. Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

The polynucleotide may have a coding sequence which is a naturally occurring
10 allelic variant of the coding sequence characterized by the DNA sequence disclosed herein. As known in the art, an allelic variant is an alternate form of a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded polypeptide.

The polynucleotide which encodes for the mature polypeptide, may include only
15 the coding sequence for the mature polypeptide or the coding sequence for the mature polypeptide and additional coding sequence such as a leader or secretory sequence or a proprotein sequence.

Thus, the term "polynucleotide encoding a polypeptide" encompasses a
polynucleotide which includes only coding sequence for the polypeptide as well as a
20 polynucleotide which includes additional coding and/or non-coding sequence.

The present invention therefore includes polynucleotides, wherein the coding
sequence for the mature polypeptide may be fused in the same reading frame to a
polynucleotide sequence which aids in expression and secretion of a polypeptide from a
host cell, for example, a leader sequence which functions as a secretory sequence for
25 controlling transport of a polypeptide from the cell. The polypeptide having a leader
sequence is a preprotein and may have the leader sequence cleaved by the host cell to form
the mature form of the polypeptide. The polynucleotides may also encode for a proprotein
which is the mature protein plus additional 5' amino acid residues. A mature protein having
a prosequence is a proprotein and may be an inactive form of the protein. Once the
30 prosequence is cleaved an active mature protein remains.

Thus, for example, the polynucleotide of the present invention may code for a
mature protein, or for a protein having a prosequence or for a protein having both a
prosequence and a presequence (leader sequence). Further, the amino acid sequences
provided herein show a methionine residue at the NH₂-terminus. It is appreciated, however,

that during post-translational modification of the peptide, this residue may be deleted. Accordingly, this invention contemplates the use of both the methionine-containing and the methionineless amino terminal variants of each protein disclosed herein.

The polynucleotides of the present invention may also have the coding sequence
5 fused in frame to a marker sequence at either the 5' or 3' terminus of the gene which allows for purification of the polypeptide of the present invention. The marker sequence may be a hexa-histidine tag supplied by the pQE series of vectors (supplied commercially by Quiagen Inc.) to provide for purification of the polypeptide fused to the marker in the case of a bacterial host.

10 The present invention further relates to polynucleotides which hybridize to the hereinabove-described sequences if there is at least 50% and preferably at least 70% identity between the sequences. The present invention particularly relates to polynucleotides, particularly Streptococcal polynucleotides, which hybridize under stringent conditions to the hereinabove-described polynucleotides. As herein used, the term "stringent conditions"
15 means hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences. The polynucleotides which hybridize to the hereinabove described polynucleotides in a preferred embodiment encode polypeptides which retain substantially the same biological function or activity as the polypeptide characterised by the deduced amino acid sequence given herein. An example of stringent hybridization
20 conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*,
25 Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein.

The invention also provides a polynucleotide consisting essentially of a polynucleotide sequence obtainable by screening an appropriate library containing the complete gene for a polynucleotide sequence selected from the group consisting of the
30 polynucleotides of the Sequence Listing under stringent hybridization conditions with a probe having the sequence of said polynucleotide sequence set forth in said polynucleotide of the Sequence Listing or a fragment thereof; and isolating said DNA sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers described elsewhere herein.

"Identity," as known in the art and used herein, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match

5 between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds.,

10 Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity

15 are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Atschul, S.F. et al., *J. Molec. Biol.* 215: 403-410 (1990). The BLAST X program is publicly available from NCBI and other sources (*BLAST*

20 *Manual*, Altschul, S., et al., NCBI NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990).

As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "identity" to a reference nucleotide sequence selected from the group consisting of the polynucleotide of the Sequence Listing is intended that the nucleotide

25 sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another

30 nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among

nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% identity to a reference amino acid sequence of selected from the group consisting of the amino acids of the Sequence Listing is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

The deposit referred to herein will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for purposes of Patent Procedure. These deposits are provided merely as convenience to those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained in the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with any description of sequences herein. A license may be required to make, use or sell the deposited material, and no such license is hereby granted.

The terms "fragment," "derivative" and "analogue" when referring to the polypeptide characterized by the deduced amino acid sequence herein, means a polypeptide which retains essentially the same biological function or activity as such polypeptide. Thus, an analogue includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature polypeptide.

The polypeptide of the present invention may be a recombinant polypeptide, a natural polypeptide or a synthetic polypeptide, preferably a recombinant polypeptide.

The fragment, derivative or analogue of the polypeptide characterized by the deduced amino acid sequence herein may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogues are deemed to be within the scope of those skilled in the art from the teachings herein.

The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

The present invention also relates to vectors which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques.

In accordance with yet a further aspect of the present invention, there is therefore provided a process for producing the polypeptide of the invention by recombinant techniques by expressing a polynucleotide encoding said polypeptide in a host and recovering the expressed product. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a cosmid, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the

genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

Suitable expression vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable and viable in the host.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the *E. coli* *lac* or *trp*, the phage lambda P_L promoter and other promoters known to control expression of genes in eukaryotic or prokaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

The gene can be placed under the control of a promoter, ribosome binding site (for bacterial expression) and, optionally, an operator (collectively referred to herein as "control" elements), so that the DNA sequence encoding the desired protein is transcribed into RNA in the host cell transformed by a vector containing this expression construction. The coding sequence may or may not contain a signal peptide or leader sequence. The polypeptides of the present invention can be expressed using, for example, the *E. coli* *tac* promoter or the protein A gene (*spa*) promoter and signal sequence. Leader sequences can be removed by the bacterial host in post-translational processing. See, e.g., U.S. Patent Nos. 4,431,739; 4,425,437; 4,338,397. Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are PKK232-8 and PCM7. Particular named bacterial promoters include *lacI*, *lacZ*, T3, T7, *gpt*, lambda P_R , P_L and *trp*. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and

mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

In addition to control sequences, it may be desirable to add regulatory sequences which allow for regulation of the expression of the protein sequences relative to the growth of the host cell. Regulatory sequences are known to those of skill in the art, and examples include those which cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Other types of regulatory elements may also be present in the vector, for example, enhancer sequences.

10 An expression vector is constructed so that the particular coding sequence is located in the vector with the appropriate regulatory sequences, the positioning and orientation of the coding sequence with respect to the control sequences being such that the coding sequence is transcribed under the "control" of the control sequences (i.e., RNA polymerase which binds to the DNA molecule at the control sequences transcribes the coding
15 sequence). Modification of the coding sequences may be desirable to achieve this end. For example, in some cases it may be necessary to modify the sequence so that it may be attached to the control sequences with the appropriate orientation; i.e., to maintain the reading frame. The control sequences and other regulatory sequences may be ligated to the coding sequence prior to insertion into a vector, such as the cloning vectors described
20 above. Alternatively, the coding sequence can be cloned directly into an expression vector which already contains the control sequences and an appropriate restriction site.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-
25 expressed gene to direct transcription of a downstream structural sequence. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal
30 identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this
5 embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pET-3 vectors (Stratagene), pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks,
10 pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pBlueBacIII (Invitrogen), pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

15 Examples of recombinant DNA vectors for cloning and host cells which they can transform include the bacteriophage λ (*E. coli*), pBR322 (*E. coli*), pACYC177 (*E. coli*), pKT230 (gram-negative bacteria), pGV1106 (gram-negative bacteria), pLAFR1 (gram-negative bacteria), pME290 (non-*E. coli* gram-negative bacteria), pHV14 (*E. coli* and *Bacillus subtilis*), pBD9 (*Bacillus*), pIJ61 (*Streptomyces*), pUC6 (*Streptomyces*), YIp5
20 (*Saccharomyces*), a baculovirus insect cell system, YCp19 (*Saccharomyces*). See, generally, "DNA Cloning": Vols. I & II, Glover *et al.* ed. IRL Press Oxford (1985) (1987) and; T. Maniatis *et al.* ("Molecular Cloning" Cold Spring Harbor Laboratory (1982).

In some cases, it may be desirable to add sequences which cause the secretion of the polypeptide from the host organism, with subsequent cleavage of the secretory signal.

25 Polypeptides can be expressed in host cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold
30 Spring Harbor, N.Y., (1989), the disclosure of which is hereby incorporated by reference.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use
5 of cell lysing agents, such methods are well known to those skilled in the art.

Depending on the expression system and host selected, the polypeptide of the present invention may be produced by growing host cells transformed by an expression vector described above under conditions whereby the polypeptide of interest is expressed. The polypeptide is then isolated from the host cells and purified. If the expression system
10 secretes the polypeptide into growth media, the polypeptide can be purified directly from the media. If the polypeptide is not secreted, it is isolated from cell lysates or recovered from the cell membrane fraction. Where the polypeptide is localized to the cell surface, whole cells or isolated membranes can be used as an assayable source of the desired gene product. Polypeptide expressed in bacterial hosts such as *E. coli* may require isolation from
15 inclusion bodies and refolding. Where the mature protein has a very hydrophobic region which leads to an insoluble product of overexpression, it may be desirable to express a truncated protein in which the hydrophobic region has been deleted. The selection of the appropriate growth conditions and recovery methods are within the skill of the art.

The polypeptide can be recovered and purified from recombinant cell cultures by
20 methods including ammonium sulphate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography
25 (HPLC) can be employed for final purification steps.

Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. Polypeptides of the invention may also include an initial methionine amino acid residue.

A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that
30 functions as an autonomous unit of DNA replication *in vivo*; i.e., capable of replication under its own control.

A "vector" is a replicon, such as a plasmid, phage, or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

A "double-stranded DNA molecule" refers to the polymeric form of deoxyribonucleotides (bases adenine, guanine, thymine, or cytosine) in a double-stranded helix, both relaxed and supercoiled. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter alia*, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of DNA (i.e., the strand having the sequence homologous to the mRNA).

A DNA "coding sequence of" or a "nucleotide sequence encoding" a particular protein, is a DNA sequence which is transcribed and translated into a polypeptide when placed under the control of appropriate regulatory sequences.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bound at the 3' terminus by a translation start codon (e.g., ATG) of a coding sequence and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

DNA "control sequences" refers collectively to promoter sequences, ribosome binding sites, polyadenylation signals, transcription termination sequences, upstream regulatory domains, enhancers, and the like, which collectively provide for the expression (i.e., the transcription and translation) of a coding sequence in a host cell.

A control sequence "directs the expression" of a coding sequence in a cell when RNA polymerase will bind the promoter sequence and transcribe the coding sequence into mRNA, which is then translated into the polypeptide encoded by the coding sequence.

A "host cell" is a cell which has been transformed or transfected, or is capable of transformation or transfection by an exogenous DNA sequence.

A cell has been "transformed" by exogenous DNA when such exogenous DNA has been introduced inside the cell membrane. Exogenous DNA may or may not be integrated (covalently linked) into chromosomal DNA making up the genome of the cell. In prokaryotes and yeasts, for example, the exogenous DNA may be maintained on an episomal element, such as a plasmid. With respect to eukaryotic cells, a stably transformed or transfected cell is one in which the exogenous DNA has become integrated into the chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cell containing the exogenous DNA.

5 A "clone" is a population of cells derived from a single cell or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

10 A "heterologous" region of a DNA construct is an identifiable segment of DNA within or attached to another DNA molecule that is not found in association with the other molecule in nature.

15 This invention is also related to the use of the polynucleotides of the invention for use as diagnostic reagents. Detection of a polynucleotide or polypeptide of the invention in a eukaryote, particularly a mammal, and especially a human, will provide a diagnostic method for diagnosis of a disease. Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with an organism comprising a polynucleotide of the invention may be detected at the nucleic acid level by a variety of techniques.

20 Nucleic acids for diagnosis may be obtained from an infected individual's cells and tissues, such as bone, blood, muscle, cartilage, and skin. Genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR or other amplification technique prior to analysis. RNA or cDNA may also be used in the same ways. Using amplification, characterization of the species and strain of prokaryote present in an individual, may be made by an analysis of the genotype of the prokaryote gene. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the genotype of a reference sequence. Point mutations can be identified by hybridizing amplified DNA to labeled polynucleotide sequences of the invention. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence differences may also be detected by alterations in the electrophoretic mobility of the DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing. See, *e.g.*, Myers et al., *Science*, 230: 1242 (1985). Sequence changes at specific locations also may be

revealed by nuclease protection assays, such as RNase and S1 protection or a chemical cleavage method. See, e.g., Cotton et al., *Proc. Natl. Acad. Sci., USA*, 85: 4397-4401 (1985).

5 Cells carrying mutations or polymorphisms in the gene of the invention may also be detected at the DNA level by a variety of techniques, to allow for serotyping, for example. For example, RT-PCR can be used to detect mutations. It is particularly preferred to use RT-PCR in conjunction with automated detection systems, such as, for example, GeneScan. RNA or cDNA may also be used for the same purpose, PCR or RT-PCR. As an example, PCR primers complementary to a nucleic acid encoding a polypeptide of the invention can be used to identify
10 and analyze mutations. These primers may be used for, among other things, amplifying DNA isolated from a sample derived from an individual. The primers may be used to amplify the gene isolated from an infected individual such that the gene may then be subject to various techniques for elucidation of the DNA sequence. In this way, mutations in the DNA sequence may be detected and used to diagnose infection and to serotype and/or classify the infectious agent.

15 The invention further provides a process for diagnosing disease, preferably bacterial infections, more preferably infections by *Streptococcus pneumoniae*, comprising determining from a sample derived from an individual a increased level of expression of polynucleotide having a sequence set forth in the Sequence Listing or a sequence of the invention. Increased or decreased expression of a polynucleotide of the invention can be measured
20 using any one of the methods well known in the art for the quantitation of polynucleotides, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods.

In addition, a diagnostic assay in accordance with the invention for detecting over-expression of a polypeptide of the invention compared to normal control tissue samples may be
25 used to detect the presence of an infection, for example. Assay techniques that can be used to determine levels of a polypeptide of the invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

In accordance with yet a further aspect of the present invention, there is provided
30 the use of a polypeptide of the invention for therapeutic or prophylactic purposes, for example, as an antibacterial agent or a vaccine.

In accordance with another aspect of the present invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunisation.

In accordance with yet another aspect of the present invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents. In particular, there are provided antibodies against such polypeptides.

Polypeptides of the invention may also be used to assess the binding of small molecule
5 substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates and ligands or may be structural or functional mimetics. See, *e.g.*, Coligan *et al.*, *Current Protocols in Immunology* 1(2): Chapter 5 (1991).

The invention also provides a method of screening compounds to identify those which
10 enhance (agonist) or block (antagonist) the action of polypeptides or polynucleotides of the invention, particularly those compounds that are bacteriostatic and/or bacteriocidal. The method of screening may involve high-throughput techniques. For example, to screen for agonists or antagonists, a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, comprising a polypeptide of the invention and a
15 labeled substrate or ligand of such polypeptide is incubated in the absence or the presence of a candidate molecule that may be an agonist or antagonist of a polypeptide of the invention. The ability of the candidate molecule to agonize or antagonize a polypeptide of the invention is reflected in decreased binding of the labeled ligand or decreased production of product from such substrate. Molecules that bind gratuitously, *i.e.*, without inducing the effects of a polypeptide of
20 the invention are most likely to be good antagonists. Molecules that bind well and increase the rate of product production from substrate are agonists. Detection of the rate or level of production of product from substrate may be enhanced by using a reporter system. Reporter systems that may be useful in this regard include but are not limited to colorimetric labeled substrate converted into product, a reporter gene that is responsive to changes in polynucleotide or
25 polypeptide activity, and binding assays known in the art.

Another example of an assay for antagonists of a polypeptide of the invention is a competitive assay that combines such polypeptide and a potential antagonist with polypeptide-binding molecules, recombinant polypeptide-binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay.
30 Polypeptides of the invention can be labeled, such as by radioactivity or a colorimetric compound, such that the number of such polypeptide molecules bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a polynucleotide or polypeptide of the invention and thereby inhibit or extinguish its activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, without inducing an activities of a polypeptide of the invention, thereby preventing the action of such polypeptide by excluding it from binding.

Potential antagonists include a small molecule that binds to and occupies the binding site of the polypeptide thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules (see Okano, *J. Neurochem.* 56: 560 (1991); *OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION*, CRC Press, Boca Raton, FL (1988), for a description of these molecules). Preferred potential antagonists include compounds related to and variants of the polypeptides of the invention.

Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein, upon expression, can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The invention also provides the use of the polypeptide, polynucleotide or inhibitor of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: in the prevention of adhesion of bacteria, in particular gram positive bacteria, to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block protein-mediated mammalian cell invasion by, for example, initiating phosphorylation of mammalian tyrosine kinases (Rosenshine *et al.*, *Infect. Immun.* 60:2211 (1992); to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins that mediate tissue damage and; to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

The antagonists and agonists of the invention may be employed, for instance, to inhibit and treat otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural

empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid.

Another aspect of the invention is a pharmaceutical composition comprising the above polypeptide, polynucleotide or inhibitor of the invention and a pharmaceutically acceptable carrier.

In a particular aspect the invention provides the use of an inhibitor of the invention as an antibacterial agent.

The invention further relates to the manufacture of a medicament for such uses.

The polypeptide may be used as an antigen for vaccination of a host to produce specific antibodies which have anti-bacterial action. This invention also contemplates the use of the DNA encoding the antigen as a component in a DNA vaccine as discussed more fully below.

The polypeptides or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal antibodies. The term antibodies also includes chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

Antibodies generated against the polypeptides of the present invention can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind the polypeptides itself. In this manner, even a sequence encoding only a fragment of the polypeptides can be used to generate antibodies binding the whole native polypeptides. Such antibodies can then be used to isolate the polypeptide from tissue expressing that polypeptide.

Polypeptide derivatives include antigenically or immunologically equivalent derivatives which form a particular aspect of this invention.

The term 'antigenically equivalent derivative' as used herein encompasses a polypeptide or its equivalent which will be specifically recognised by certain antibodies which, when raised to the protein or polypeptide according to the present invention, interfere with the interaction between pathogen and mammalian host.

The term 'immunologically equivalent derivative' as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a

vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

In particular derivatives which are slightly longer or slightly shorter than the native protein or polypeptide fragment of the present invention may be used. In addition,
5 polypeptides in which one or more of the amino acid residues are modified may be used. Such peptides may, for example, be prepared by substitution, addition, or rearrangement of amino acids or by chemical modification thereof. All such substitutions and modifications are generally well known to those skilled in the art of peptide chemistry.

The polypeptide, such as an antigenically or immunologically equivalent derivative
10 or a fusion protein thereof is used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the polypeptide. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively a multiple antigenic peptide comprising multiple copies of the protein or
15 polypeptide, or an antigenically or immunologically equivalent polypeptide thereof may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, *Nature*, 256:495-497(1975)), the trioma technique, the
20 human B-cell hybridoma technique (Kozbor et al., *Immunology Today* 4:72(1983)), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole, et al., 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96).

Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptide
25 products of this invention.

Using the procedure of Kohler and Milstein (*supra*, (1975)), antibody-containing cells from the immunised mammal are fused with myeloma cells to create hybridoma cells secreting monoclonal antibodies.

The hybridomas are screened to select a cell line with high binding affinity and
30 favorable cross reaction with other Streptococcal species using one or more of the original polypeptide and/or the fusion protein. The selected cell line is cultured to obtain the desired Mab.

Hybridoma cell lines secreting the monoclonal antibody are another aspect of this invention.

Alternatively phage display technology could be utilised to select antibody genes with binding activities towards the polypeptide either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing anti-Fbp or from naive libraries (McCafferty, J. *et al.*, Nature 348:552-554(1990), and Marks, J. *et al.*, Biotechnology 10:779-783(1992)). The affinity of these antibodies can also be improved by chain shuffling (Clackson, T. *et al.*, Nature 352:624-628(1991)).

The antibody should be screened again for high affinity to the polypeptide and/or fusion protein.

As mentioned above, a fragment of the final antibody may be prepared.

10 The antibody may be either intact antibody of M_r approx 150,000 or a derivative of it, for example a Fab fragment or a Fv fragment as described in Skerra, A and Pluckthun, A., Science 240:1038-1040 (1988). If two antigen binding domains are present each domain may be directed against a different epitope - termed 'bispecific' antibodies.

15 The antibody of the invention may be prepared by conventional means for example by established monoclonal antibody technology (Kohler, G. and Milstein, C. (*supra*, (1975) or using recombinant means e.g. combinatorial libraries, for example as described in Huse, W.D. *et al.*, Science 246:1275-1281 (1989).

20 Preferably the antibody is prepared by expression of a DNA polymer encoding said antibody in an appropriate expression system such as described above for the expression of polypeptides of the invention. The choice of vector for the expression system will be determined in part by the host, which may be a prokaryotic cell, such as *E. coli* (preferably strain B) or *Streptomyces sp.* or a eukaryotic cell, such as a mouse C127, mouse myeloma, human HeLa, Chinese hamster ovary, filamentous or unicellular fungi or insect cell. The host may also be a transgenic animal or a transgenic plant (for example, as described in 25 Hiatt, A. *et al.*, Nature 340:76-78(1989). Suitable vectors include plasmids, bacteriophages, cosmids and recombinant viruses, derived from, for example, baculoviruses and vaccinia.

The Fab fragment may also be prepared from its parent monoclonal antibody by enzyme treatment, for example using papain to cleave the Fab portion from the Fc portion.

30 Preferably the antibody or derivative thereof is modified to make it less immunogenic in the patient. For example, if the patient is human the antibody may most preferably be 'humanised'; where the complementarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in Jones, P. *et al.*, Nature 321:522-525 (1986), or Tempest *et al.*, Biotechnology 9:266-273 (1991).

The modification need not be restricted to one of 'humanisation'; other primate sequences (for example Newman, R. *et al.*, Biotechnology 10:1455-1460 (1992)) may also be used.

The humanised monoclonal antibody, or its fragment having binding activity, form
5 a particular aspect of this invention.

This invention provides a method of screening drugs to identify those which interfere with the proteins selected as targets herein, which method comprises measuring the interference of the activity of the protein by a test drug. For example if the protein selected has a catalytic activity, after suitable purification and formulation the activity of the enzyme
10 can be followed by its ability to convert its natural substrates. By incorporating different chemically synthesised test compounds or natural products into such an assay of enzymatic activity one is able to detect those additives which compete with the natural substrate or otherwise inhibit enzymatic activity.

The invention also relates to inhibitors identified thereby.

15 The use of a polynucleotide of the invention in genetic immunisation will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscles (Wolff *et al.*, Hum. Mol. Genet. 1:363 (1992); Manthorpe *et al.*, Hum. Gene Ther. 4:419 (1993)), delivery of DNA complexed with specific protein carriers (Wu *et al.*, J. Biol. Chem. 264:16985 (1989)), coprecipitation of DNA with calcium phosphate
20 (Benvenisty & Reshef, Proc. Nat'l Acad. Sci. USA, 83:9551 (1986)), encapsulation of DNA in various forms of liposomes (Kaneda *et al.*, Science 243:375 (1989)), particle bombardment (Tang *et al.*, Nature 356:152 (1992)); Eisenbraun *et al.*, DNA Cell Biol. 12:791 (1993)) and *in vivo* infection using cloned retroviral vectors (Seeger *et al.*, Proc. Nat'l. Acad. Sci. USA 81:5849 (1984)). Suitable promoters for muscle transfection include
25 CMV, RSV, SRa, actin, MCK, alpha globin, adenovirus and dihydrofolate reductase.

In therapy or as a prophylactic, the active agent i.e., the polypeptide, polynucleotide or inhibitor of the invention, may be administered to a patient as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application
30 for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol

or oleyl alcohol for lotions. Such carriers may constitute from about 1% to about 98% by weight of the formulation; more usually they will constitute up to about 80% by weight of the formulation.

5 For administration to human patients, it is expected that the daily dosage level of the active agent will be from 0.01 to 10 mg/kg, typically around 1 mg/kg. The physician in any event will determine the actual dosage which will be most suitable for an individual patient and will vary with the age, weight and response of the particular patient. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this
10 invention.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response.

A suitable unit dose for vaccination is 0.5-5 μ g/kg of antigen, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

15 Within the indicated dosage range, no adverse toxicological effects are expected with the compounds of the invention which would preclude their administration to suitable patients.

In order to facilitate understanding of the following example certain frequently occurring methods and/or terms will be described.

20 "Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

25 "Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 μ g of plasmid or DNA fragment is used with about 2 units of enzyme
30 in about 20 μ l of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 μ g of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37° C are ordinarily

used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

Size separation of the cleaved fragments is performed using 8 percent polyacrylamide gel described by Goeddel, D. *et al.*, (1980) *Nucleic Acids Res.*, 8:4057.

5 "Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

10 "Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Maniatis, T., *et al.*, *supra*, p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units to T4 DNA ligase ("ligase") per 0.5 µg of approximately equimolar amounts of the DNA fragments to be ligated.

15 Example 1

Isolation of DNA coding for a virulence gene in *Streptococcus pneumoniae*

As mentioned above each of the DNAs disclosed herein by virtue of the fact that it includes an intact open reading frame is useful to a greater or lesser extent as a screen for identifying antimicrobial compounds. A useful approach for selecting the preferred DNA
20 sequences for screen development is evaluation by insertion-duplication mutagenesis. This system disclosed by Morrison *et al.*, *J. Bacteriol.* 159:870 (1984), is applied as follows.

Briefly, random fragments of *Streptococcus pneumoniae*, strain 0100993 DNA are generated enzymatically (by restriction endonuclease digestion) or physically (by sonication based shearing) followed by gel fractionation and end repair employing T4 DNA
25 polymerase. It is preferred that the DNA fragments so produced are in the range of 200-400 base pairs, a size sufficient to ensure homologous recombination and to insure a representative library in *E. coli*. The fragments are then inserted into appropriately tagged plasmids as described in Hensel *et al.*, *Science* 269: 400-403(1995). Although a number of plasmids can be used for this purpose, a particularly useful plasmid is pJDC9 described by
30 Pearce *et al.*, *Mol. Microbiol.* 9:1037 (1993) which carries the *erm* gene facilitating erythromycin selection in either *E. coli* or *S. pneumoniae* previously modified by incorporation of DNA sequence tags into one of the polylinker cloning sites. The tagged plasmids are introduced into the appropriate *S. pneumoniae* strain selected, *inter alia*, on the basis of serotype and virulence in a murine model of pneumococcal pneumonia.

It is appreciated that a seventeen amino acid competence factor exists (Havastein et al., Proc. Nat'l. Acad. Sci. USA 92:11140-44 (1995)) and may be usefully employed in this protocol to increase the transformation frequencies. A proportion of transformants are analysed to verify homologous integration and as a check on stability. Unwanted levels of reversion are minimized because the duplicated regions will be short (200-400 bp), however if significant reversion rates are encountered they may be modulated by maintaining antibiotic selection during the growth of the transformants in culture and/or during growth in the animal.

The *S. pneumoniae* transformants are pooled for inoculation into mice, eg., Swiss and/or C57B1/6. Preliminary experiments are conducted to establish the optimum complexity of the pools and level of inoculum. A particularly useful model has been described by Veber et al. (J. Antimicrobiol. Chemother. 32:432 (1993) in which 10^5 cfu inocula sizes are introduced by mouth to the trachea. Strain differences are observed with respect to onset of disease e.g., 3-4 days for Swiss mice and 8-10 days for C57B1/6. Infection yields in the lungs approach 10^8 cfu/lung. IP administration is also possible when genes mediating blood stream infection are evaluated. Following optimization of parameters of the infection model, the mutant bank normally comprising several thousand strains is subjected to the virulence test. Mutants with attenuated virulence are identified by hybridization analysis using the labelled tags from the "input" and "recovered" pools as probes as described in Hensel et al., Science 269: 400-403(1995). *S. pneumoniae* DNA is colony blotted or dot blotted, DNA flanking the integrated plasmid is cloned by plasmid rescue in *E. coli* (Morrison et al., J. Bacteriol. 159:870 (1984)) and sequenced. Following sequencing, the DNA is compared to the nucleotide sequences given herein and the appropriate ORF is identified and function confirmed for example by knock-out studies. Expression vectors providing the selected protein are prepared and the protein is configured in an appropriate screen for the identification of anti-microbial agents. Alternatively, genomic DNA libraries are probed with restriction fragments flanking the integrated plasmid to isolate full-length cloned virulence genes whose function can be confirmed by "knock-out" studies or other methods, which are then expressed and incorporated into a screen as described above.

The individual full length sequences given herein are summarized in the following Tables (Table 1 and Table 2). Under the column in Table 1 labeled "Identity" there is the deduced identity of each open reading frame of the invention determined using Blastp and/or MPSearch. The ORF# column indicates whether the polynucleotide encoding each

ORF encodes more than one ORF. For example, SEQ ID NO:224 has an ORF# 1 but no #2; thus the polynucleotide encodes this ORF#1, but no other ORF was detected. On the other hand, SEQ ID NO:225 and 226 have ORF#s 1 and 2 respectively, indicating that they were both encoded by the same polynucleotide. This can also be seen in Table 2 where the polynucleotide of SEQ ID NO: 2 encodes the ORFs of SEQ ID NOS: 225 and 226. Table 1 also shows the start ("START" column) and stop ("STOP" column) codons for each ORF and their positions in the encoding polynucleotide sequence. The SEQ ID NOS of the polypeptides of this table are linked to both a deduced identity in this table and a polynucleotide sequence in Table 2 which encodes each polypeptide. The "Direction" column in Table 1 shows the direction of the ORF encoding each polypeptide in this table. "Forward" denotes the sense orientation and "Reverse" denotes the antisense orientation of the ORF.

TABLE 1

| SEQ ID NO: | Identity | ORF # | Codon | | Position | | Direction |
|------------|--|-------|-------|------|----------|------|-----------|
| | | | Start | Stop | Start | Stop | |
| 224. | Phosphate Transport ATP-Binding Protein PSTB. - <i>Escherichia</i> | 1 | -CAT | TCA- | 2 | 553 | Reverse |
| 225. | probable ATP binding protein - <i>Bacillus subtilis</i> | 1 | -CAT | TCA- | 38 | 781 | Reverse |
| 226. | Nopaline Transport System Permease Protein Nocr. - <i>Agrobacterium Tumefaciens</i> | 2 | -CAG | TTA- | 781 | 1512 | Reverse |
| 227. | Aspartate Aminotransferase A (EC 2.6.11) (Transaminase A) (ASPAT.) - <i>Rhizobium Meliloti</i> . | 1 | ATG | TAG | 480 | 671 | Forward |
| 228. | ISL2 protein - <i>Lactobacillus helveticus</i> | 1 | ATG | TAA | 549 | 947 | Forward |
| 229. | ISL2 protein - <i>Lactobacillus helveticus</i> | 2 | ATG | TAG | 889 | 1353 | Forward |
| 230. | Unknown | 3 | ATG | TGA | 1421 | 1570 | Forward |
| 231. | Unknown | 2 | -CAT | CTA- | 111 | 413 | Reverse |
| 232. | Unknown | 1 | ATG | TGA | 133 | 282 | Forward |
| 233. | Acyl Carrier Protein (ACP.) - <i>Rhizobium Meliloti</i> . | 1 | -CAT | CTA- | 673 | 906 | Reverse |
| 234. | Unknown | 1 | -CAT | TTA- | 15 | 137 | Reverse |
| 235. | Unknown | 2 | -CAT | CTA- | 681 | 989 | Reverse |
| 236. | Sulfate Transport System Permease Protein CYST (Fragment). - <i>Synechocystis</i> SP. (Strain PCC 6803). | 2 | -CAT | TTA- | 336 | 689 | Reverse |
| 237. | probable transposase (insertion sequence IS861) - <i>Streptococcus agalactiae</i> (strain COH-1) | 2 | -CAT | TCA- | 149 | 454 | Reverse |
| 238. | Unknown | 2 | -CAG | TTA- | 567 | 851 | Reverse |
| 239. | "PTS SYSTEM | 1 | ATG | TAA | 49 | 477 | Forward |
| 240. | "PTS SYSTEM | 2 | -CAT | TTA- | 151 | 789 | Reverse |
| 241. | nitrogen fixation protein (nifS) homolog - <i>Haemophilus influenzae</i> (strain Rd KW 20) | 1 | -CAT | TCA- | 1 | 207 | Reverse |
| 242. | cellobiose phosphotransferase system celA - <i>Bacillus stearothermophilus</i> | 1 | -CAT | TCA- | 84 | 431 | Reverse |
| 243. | surface protein PspA - <i>Streptococcus pneumoniae</i> | 1 | ATG | TAA | 22 | 321 | Forward |
| 244. | Unknown | 2 | ATG | TAA | 272 | 469 | Forward |
| 245. | ATP-dependent Clp proteinase (EC 3.4.21.-) chain clpL. - <i>Lactococcus lactis</i> subs p. lactis | 1 | ATG | TGA | 83 | 760 | Forward |

| | | | | | | | |
|------|--|---|------|------|------|------|---------|
| | plasmid pUCL22 | | | | | | |
| 246. | Beta-Glucosidase (EC3.2.1.21) (Gentiobiase) (Cellobiase)) (Beta-D- Glucoside GL Ucohydrolase) (Amygdalase). - Bacillus Subtilis. | 1 | -CAT | TCA- | 153 | 599 | Reverse |
| 247. | Glycine Betaine/L-Proline Transport ATP - Binding Protein Prov. - Escherichia Col. I. | 2 | ATG | TAA | 159 | 887 | Forward |
| 248. | Unknown | 3 | -CAT | TTA- | 1102 | 1254 | Reverse |
| 249. | 30S Ribosomal Protein S11 (BS11). - Bacillus Subtilis. | 1 | ATG | TGA | 15 | 164 | Forward |
| 250. | DNA - Directed RNA Polymerase Alpha Chain (EC 2.7.7.6) (Transcriptase Alpha Chain). - Bacillus Subtilis. | 2 | ATG | TAA | 282 | 1217 | Forward |
| 251. | Peptide Chain Release Factor 3 (RF-3). - Bacteroides Nodosus (Dichelobacter Nod Osus). | 1 | ATG | TAG | 212 | 667 | Forward |
| 252. | Unknown | 1 | ATG | TAG | 267 | 353 | Forward |
| 253. | Riboflavin Synthase Alpha Chain (EC 2.5.1.9). - Bacillus Subtilis. | 2 | -CAT | CTA- | 213 | 662 | Reverse |
| 254. | Unknown | 3 | -CAT | TTA- | 833 | 1045 | Reverse |
| 255. | Unknown | 1 | -CAT | TTA- | 83 | 424 | Reverse |
| 256. | mesl protein - Leuconostoc mesenteroides | 2 | ATG | TAG | 448 | 1302 | Forward |
| 257. | Transacetylase BMTD (EC 2.3.1.-). - Bacillus Subtilis. | 1 | CTG | TAG | 3 | 320 | Forward |

| SEQ ID NO: | Identity | ORF # | Codon | Start | Stop | Position | Start | Stop | Direction |
|------------|---|-------|-------|-------|------|----------|-------|------|-----------|
| 258. | ribose-phosphate pyrophosphokinase (EC 2.7.6.1.) - <i>Bacillus caldolyticus</i> | 1 | CTG | TAG | 1 | 642 | | | Forward |
| 259. | Unknown | 1 | ATG | TAA | 66 | 614 | | | Forward |
| 260. | Unknown | 1 | ATG | TAG | 108 | 590 | | | Forward |
| 261. | nitrogenase C (nifC) homolog - <i>Haemophilus influenzae</i> (strain Rd KW20) | 2 | ATG | TAG | 631 | 855 | | | Forward |
| 262. | Unknown | 2 | ATG | TAA | 606 | 752 | | | Forward |
| 263. | Unknown | 2 | ATG | TGA | 280 | 495 | | | Forward |
| 264. | Unknown | 2 | ATG | TGA | 639 | 1466 | | | Forward |
| 265. | Acetyl Esterase (EC 3.1.-.-) - <i>Caldocellum Saccharolyticum</i> . | 2 | ATG | TAA | 274 | 594 | | | Forward |
| 266. | Unknown | 1 | -CAT | TCA- | 2 | 157 | | | Reverse |
| 267. | Triosephosphate Isomerase (EC 5.3.1.1) (TIM). - <i>Bacillus Subtilis</i> . | 1 | -CAT | TTA- | 270 | 665 | | | Reverse |
| 268. | Branched-chain Amino Acid Aminotransferase (EC 2.6.1.42) (Transaminase B). - <i>ES Chericchia Coli</i> . | 1 | ATG | TAG | 110 | 736 | | | Forward |
| 269. | branched-chain-amino-acid transaminase homolog - <i>Haemophilus influenzae</i> (strain Rd KW20) | 2 | ATG | TAA | 708 | 842 | | | Forward |
| 270. | DnaK protein - <i>Lactococcus lactis</i> | 1 | CTG | TGA | 3 | 749 | | | Forward |
| 271. | Ketol-Acid Reductoisomerase (EC 1.1.1.86) (Acetohydroxy-Acid Isomeroreductase). - <i>Lactococcus Lactis</i> (Subsp. Lactis) (<i>Streptococcus Lactis</i>) | 1 | ATG | TAA | 99 | 428 | | | Forward |
| 272. | Unknown | 1 | -CAT | CTA- | 278 | 631 | | | Reverse |
| 273. | Amidophosphoribosyltransferase Precursor (EC 2.4.2.14) (Glutamine Phosphoribosylpyrophosphate Amidotransferase) (Atase). - <i>Bacillus Subtilis</i> . | 2 | -CAT | CTA- | 152 | 775 | | | Reverse |
| 274. | Pyrrolidone-Carboxylate Peptidase (EC 3.4.19.3) (5-Oxoprolyl-Peptidase). - <i>STR Eptococcus Pvoenes</i> . | 1 | -CAT | TCA- | 156 | 803 | | | Reverse |
| 275. | 50S Ribosomal Protein L16. - <i>Mycoplasma Capricolum</i> . | 1 | ATG | TAA | 33 | 416 | | | Forward |
| 276. | serine O-acetyltransferase (EC 2.3.1.30) - <i>Bacillus stearothermophilus</i> | 2 | -CAT | CTA- | 577 | 1194 | | | Reverse |
| 277. | Unknown | 1 | ATG | TAG | 61 | 648 | | | Forward |

| | | | | | | | |
|------|--|---|------|------|-----|------|---------|
| 278. | Unknown | 1 | -CAT | CTA~ | 165 | 335 | Reverse |
| 279. | Lipoprotein Signal Peptidase (EC 3.4.23.36) (Prolipoprotein Signal Peptidase) (Signal Peptidase II) (Spase II). - <i>Staphylococcus Aureus</i> . | 1 | ATG | TAA | 56 | 517 | Forward |
| 280. | Unknown | 1 | ATG | TAA | 214 | 534 | Forward |
| 281. | Alpha-Acetolactate Decarboxylase (EC 4.1.1.5). - <i>Bacillus Subtilis</i> . | 1 | -CAT | CTA~ | 104 | 445 | Reverse |
| 282. | Dihydrodipicolinate Synthase 9EC 4.2.1.52) (DHDPS). - <i>Bacillus Subtilis</i> . | 3 | -CAT | TCA~ | 675 | 884 | Reverse |
| 283. | Polyribonucleotide Nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide Phosphorylase) (Pnpase). - <i>Photobacterium Luminescens</i> . | 1 | -CAT | TCA~ | 1 | 855 | Reverse |
| 284. | Single-Strand Binding Protein (SSB) (Helix-Destabilizing Protein). - <i>Bacillus S Ubtilis</i> | 1 | -CAT | TTA~ | 128 | 598 | Reverse |
| 285. | ATP-Dependent CLP Protease ATO-Binding Subunit CLPX. - <i>Escherichia Coli</i> . | 2 | -CAT | CTA~ | 195 | 482 | Reverse |
| 286. | ATP-Dependent CLP Protease ATO-Binding Subunit CLPX. - <i>Escherichia Coli</i> | 4 | -CAG | TCA~ | 676 | 990 | Reverse |
| 287. | N-(5'-Phosphoribosyl) Anthranilate Isomerase (EC 5.3.1.24) (PRAI). - <i>Lactococcus Lactis</i> (Subsp. Lactis) (<i>Streptococcus Lactis</i>). | 1 | ATG | TAA | 83 | 712 | Forward |
| 288. | 30S Ribosomal Protein S2. - <i>Escherichia Coli</i> . | 1 | ATG | TGA | 277 | 591 | Forward |
| 289. | 30S Ribosomal Protein S2. - <i>Escherichia Coli</i> . | 3 | ATG | TGA | 918 | 1064 | Forward |
| 290. | Possible beta-galactosidase precursor | 1 | -CAT | CTA~ | 120 | 545 | Reverse |
| 291. | Unknown | 1 | -CAT | TTA~ | 77 | 283 | Reverse |
| 292. | Unknown | 1 | -CAT | TTA~ | 1 | 198 | Reverse |
| 293. | "Phospho-2-Dehydro-3-Deoxyheptonate Aldolase | 1 | -CAT | TTA~ | 217 | 690 | Reverse |

| SEQ ID NO: | Identity | ORF # | Codon | | Position | | Direction |
|------------|--|-------|-------|------|----------|------|-----------|
| | | | Start | Stop | Start | Stop | |
| 294. | Unknown | 2 | -CAT | TTA~ | 429 | 599 | Reverse |
| 295. | Unknown | 3 | -CAT | TCA~ | 739 | 936 | Reverse |
| 296. | Sorbitol Dehydrogenase (EC 1.1.1.14) (L-Iditol 2-Dehydrogenase). - <i>Bacillus Subtilis</i> . | 1 | ATG | TAA | 64 | 480 | Forward |
| 297. | EBG Operon Repressor. - <i>Escherichia Coli</i> . | 2 | -CAT | CTA~ | 668 | 1060 | Reverse |
| 298. | cellobiose phosphotransferase system celA - <i>Bacillus stearothermophilus</i> | 2 | -CAT | TTA~ | 249 | 566 | Reverse |
| 299. | Unknown | 3 | -CAT | TCA~ | 581 | 964 | Reverse |
| 300. | Adenylosuccinate Lyase (EC 4.3.2.2) (Adenylosuccinase) (ASL). - <i>Bacillus Subtilis</i> . | 1 | -CAT | TTA~ | 99 | 809 | Reverse |
| 301. | ATP-Binding Protein BEXA. - <i>Haemophilus Influenzae</i> . | 1 | ATG | TGA | 111 | 404 | Forward |
| 302. | L-Lactate Dehydrogenase (Cytochrome) (EC 1.1.2.3). - <i>Escherichia Coli</i> . | 2 | ATG | TAA | 337 | 507 | Forward |
| 303. | Phosphate Transport System Permease Protein PSTC. - <i>Escherichia Coli</i> . | 3 | ATG | TGA | 507 | 1070 | Forward |
| 304. | Sulfate Transport ATP-Binding Protein CysA. - <i>Synechococcus SP.</i> (Strain PCC 794 2) (<i>Anacystis Nidulans R2</i>). | 1 | -CAT | CTA~ | 110 | 838 | Reverse |
| 305. | Unknown | 2 | -CAT | TTA~ | 838 | 1077 | Reverse |
| 306. | Unknown | 2 | -CAT | TCA~ | 282 | 749 | Reverse |
| 307. | Unknown | 2 | ATG | TAG | 1108 | 1290 | Forward |
| 308. | Phosphoribosylformylglycinamide Cyclo-Ligase (EC 6.3.3.1) (AIRS) (Phosphoribosyl-Aminoimidazole Synthetase) (AIR Synthase). - <i>Bacillus Subtilis</i> . | 2 | -CAT | TCA~ | 331 | 477 | Reverse |
| 309. | Unknown | 2 | ATG | TAA | 313 | 765 | Forward |
| 310. | SMS Protein. - <i>Escherichia Coli</i> . | 1 | -CAT | TCA~ | 102 | 416 | Reverse |
| 311. | sigma 42 protein - <i>Enterococcus faecalis</i> | 1 | -CAT | TCA~ | 8 | 487 | Reverse |
| 312. | Unknown | 1 | -CAT | TTA~ | 76 | 390 | Reverse |
| 313. | Guanylate Kinase (EC 2.7.4.8) (GMP Kinase). - <i>Escherichia Coli</i> . | 2 | -CAG | TTA~ | 415 | 849 | Reverse |
| 314. | Unknown | 1 | -CAT | TCA~ | 51 | 296 | Reverse |
| 315. | Unknown | 1 | ATG | TAA | 175 | 285 | Forward |
| 316. | Unknown | 2 | ATG | TAA | 361 | 558 | Forward |
| 317. | Unknown | 3 | ATG | TAA | 383 | 1144 | Forward |

| | | | | | | | |
|------|---|---|------|------|-----|------|---------|
| 318. | "PTS System | 2 | -CAT | TCA~ | 166 | 465 | Reverse |
| 319. | L-Fucose Isomerase (EC 5.3.1.-) - Escherichia Coli. | 1 | -CAT | CTA~ | 9 | 482 | Reverse |
| 320. | Unknown | 2 | -CAT | TTA~ | 495 | 650 | Reverse |
| 321. | Unknown | 1 | ATG | TGA~ | 130 | 231 | Forward |
| 322. | 3-Oxoacyl-[Acyl-Carrier Protein] Reductase (EC 1.1.1.100) (3-Ketoacyl- Acyl Car Rier Protein Reductase). - Escherichia Coli. | 1 | -CAT | TCA~ | 51 | 200 | Reverse |
| 323. | 3-Oxoacyl-[Acyl-Carrier Protein] Reductase (EC 1.1.1.100) (3-Ketoacyl- Acyl Car Rier Protein Reductase). - Escherichia Coli. | 2 | -CAT | TCA~ | 231 | 614 | Reverse |
| 324. | 2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alph A- IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis). | 1 | -CAT | TTA~ | 31 | 231 | Reverse |
| 325. | 2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alph A- IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis). | 2 | -CAT | TCA~ | 191 | 334 | Reverse |
| 326. | Unknown | 3 | -CAT | TCA~ | 309 | 452 | Reverse |
| 327. | 2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alph A- IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis). | 4 | -CAT | TTA~ | 495 | 1127 | Reverse |
| 328. | Unknown | 2 | -CAT | TCA~ | 170 | 469 | Reverse |
| 329. | Unknown | 1 | ATG | TAG | 105 | 473 | Forward |
| 330. | Strscaa Ncbi gi: 310629NCBI gi: 473 - Streptococcus gordonii (strain PK488) DNA | 1 | -CAG | CTA~ | 81 | 665 | Reverse |

| SEQ ID NO: | Identity | ORF # | Codon | | Position | | Direction |
|------------|---|-------|-------|------|----------|------|-----------|
| | | | Start | Stop | Start | Stop | |
| 331. | Unknown | 1 | ATG | TGA | 228 | 374 | Forward |
| 332. | lysyl aminopeptidase (EC 3.4.11.15) precursor - <i>Lactococcus lactis</i> | 1 | -CAT | TCA~ | 107 | 766 | Reverse |
| 333. | Indole-3-Glycerol Phosphate Synthase (EC 4.1.1.48) (IGPS). - <i>Lactococcus Lactis</i> (SUBSP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>) | 1 | -CAT | TCA~ | 127 | 369 | Reverse |
| 334. | Anthranilate Phosphoribosyltransferase (EC 2.4.2.18).- <i>Lactococcus Lactis</i> (Sub SP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>). | 2 | -CAA | TCA~ | 366 | 641 | Reverse |
| 335. | Tagatose-6-Phosphate Kinase (EC 2.7.1.-) (Phosphotagatokinase). - <i>Lactococcus L. Actis</i> (Subsp. <i>Lactis</i>) (<i>Streptococcus Lactis</i>) | 1 | ATG | TGA | 42 | 524 | Forward |
| 336. | Unknown | 1 | ATG | TGA | 73 | 474 | Forward |
| 337. | Unknown | 1 | -CAT | TTA~ | 32 | 286 | Reverse |
| 338. | Unknown | 1 | ATG | TGA | 306 | 572 | Forward |
| 339. | Acetolactate Synthase Large Subunit (EC 4.1.3.18) (AHAS) (Acetphydroxy-Acid Synthase Large Subunit) (ALS). - <i>Lactococcus Lactis</i> (SUBSP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>). | 1 | ATG | TAG | 59 | 502 | Forward |
| 340. | Penicillin-Binding Proteins 1A/1B. - <i>Bacillus Subtilis</i> . | 2 | ATG | TGA | 535 | 720 | Forward |
| 341. | Unknown | 1 | ATG | TAG | 165 | 488 | Forward |
| 342. | Anthranilate Phosphoribosyltransferase (EC 2.4.2.18). - <i>Lactococcus Lactis</i> (SUB SP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>). | 1 | -CAT | TCA~ | 5 | 394 | Reverse |
| 343. | grpE protein - <i>Lactococcus Lactis</i> | 2 | ATG | TAA | 124 | 543 | Forward |
| 344. | Unknown | 1 | -CAT | CTA~ | 34 | 195 | Reverse |
| 345. | Unknown | 2 | -CAT | TTA~ | 377 | 544 | Reverse |
| 346. | Unknown | 2 | ATG | TAA | 159 | 503 | Forward |
| 347. | Unknown | 2 | -CAT | CTA~ | 315 | 644 | Reverse |
| 348. | Unknown | 2 | -CAT | CTA~ | 468 | 587 | Reverse |
| 349. | Unknown | 2 | -CAT | CTA~ | 482 | 631 | Reverse |
| 350. | Unknown | 2 | -CAT | TTA~ | 380 | 757 | Reverse |
| 351. | NIFS Protein Homolog (Fragment). - <i>Lactobacillus Delbrueckii</i> (SUBSP. <i>Bulgaricus</i>). | 1 | ATG | TAG | 87 | 797 | Forward |
| 352. | "Ornithine Carbamoyltransferase | 1 | TTG | TAA | 2 | 502 | Forward |

| | | | | | | | |
|------|---|---|------|------|-----|-----|---------|
| 353. | PSEGLI NCBI gi: 499660 - <i>Pseudomonas putida</i> . | 1 | -CAT | TTA~ | 50 | 481 | Reverse |
| 354. | Unknown | 1 | CTG | TAA | 1 | 522 | Forward |
| 355. | Thioredoxin. - <i>Streptomyces Clavuligerus</i> . | 1 | ATG | TAG | 58 | 375 | Forward |
| 356. | D-alanine permease (dagA) homolog - <i>Haemophilus influenzae</i> (strain Rd KW20) | 1 | ATG | TAG | 185 | 343 | Forward |
| 357. | Unknown | 1 | -CAT | TTA~ | 78 | 371 | Reverse |
| 358. | "DNA Polymerase III | 1 | -CAA | TCA~ | 82 | 561 | Reverse |
| 359. | Transport ATP-Binding Protein Coma. - <i>Streptococcus Pneumoniae</i> . | 1 | -CAT | TTA~ | 112 | 552 | Reverse |
| 360. | Unknown | 2 | ATG | TAA | 445 | 540 | Forward |
| 361. | surface protein PspA - <i>Streptococcus pneumoniae</i> | 1 | -CAT | TCA~ | 45 | 416 | Reverse |
| 362. | Licid Protein. - <i>Haemophilus Influenzae</i> | 2 | ATG | TAA | 268 | 633 | Forward |
| 363. | Unknown | 2 | ATG | TAA | 527 | 640 | Forward |
| 364. | Glutamine Transport ATP- Binding Protein GLNQ. - <i>Escherichia Coli</i> . | 1 | CTG | TGA | 1 | 393 | Forward |
| 365. | Unknown | 1 | ATG | TAG | 184 | 303 | Forward |
| 366. | Unknown | 1 | ATG | TGA | 794 | 919 | Forward |
| 367. | Lipoamide Dehydrogenase Component (E3) of Pyruvate Dehydrogenase Complex (EC 1.8.1.4) (Dihydrolipoamide Dehydrogenase). - <i>Azotobacter Vinelandii</i> . | 1 | ATG | TAA | 3 | 416 | Forward |

| SEQ ID NO: | Identity | ORF # | Codon | | Position | | Direction |
|------------|--|-------|-------|------|----------|------|-----------|
| | | | Start | Stop | Start | Stop | |
| 368. | Orotate Phosphoribosyltransferase (EC 2.4.2.10) (OPRT). - <i>Bacillus Subtilis</i> . | 1 | -CAT | CTA~ | 21 | 311 | Reverse |
| 369. | Unknown | 1 | ATG | TAA | 28 | 309 | Forward |
| 370. | SPO0B-Associated GTP-Binding Protein. - <i>Bacillus Subtilis</i> . | 1 | ATG | TGA | 110 | 538 | Forward |
| 371. | Transport ATP-Binding Protein COMA. - <i>Streptococcus Pneumoniae</i> . | 1 | -CAA | TCA~ | 47 | 679 | Reverse |
| 372. | prephenate dehydrogenase (EC 1.3.1.12) - <i>Lactococcus lactis</i> . | 2 | ATG | TAG | 271 | 492 | Forward |
| 373. | O-Sialoglycoprotein Endopeptidase (EC 3.4.24.57) (Glycoprotease). - <i>Pasteurella Haemolytica</i> . | 1 | CTG | TAA | 1 | 450 | Forward |
| 374. | Unknown | 1 | -CAT | TTA~ | 7 | 282 | Reverse |
| 375. | Unknown | 1 | TTG | TAA | 2 | 265 | Forward |
| 376. | "DNA Polymerase III | 1 | ATG | TGA | 3 | 401 | Forward |
| 377. | Unknown | 2 | ATG | TAA | 361 | 516 | Forward |
| 378. | Dihydrodipicolinate Synthase (EC 4.2.1.52) (DHDPS). - <i>Bacillus Subtilis</i> . | 1 | -CAT | TTA~ | 179 | 457 | Reverse |
| 379. | Unknown | 2 | -CAT | TCA~ | 104 | 322 | Reverse |
| 380. | Unknown | 2 | -CAT | TCA~ | 248 | 649 | Reverse |
| 381. | Unknown | 1 | -CAT | TTA~ | 56 | 394 | Reverse |
| 382. | Unknown | 2 | -CAT | TTA~ | 254 | 409 | Reverse |
| 383. | Unknown | 1 | ATG | TAG | 138 | 617 | Forward |
| 384. | Unknown | 2 | -CAT | TTA~ | 225 | 479 | Reverse |
| 385. | Unknown | 2 | ATG | TAA | 747 | 857 | Forward |
| 386. | Unknown | 1 | ATG | TAG | 294 | 443 | Forward |
| 387. | Unknown | 2 | ATG | TGA | 356 | 544 | Forward |
| 388. | Unknown | 1 | -CAT | CTA~ | 4 | 141 | Reverse |
| 389. | Unknown | 1 | CTG | TAG | 1 | 579 | Forward |
| 390. | Unknown | 2 | -CAT | TTA~ | 309 | 452 | Reverse |
| 391. | Phosphopentomutase (EC 5.4.2.7). - <i>Escherichia Coli</i> . | 1 | ATG | TAA | 3 | 233 | Forward |
| 392. | D-Alanyl-D-Alanine Carboxypeptidase Precursor (EC 3.4.16.4) (DD-Peptidase)(DD - Carboxypeptidase)(Cpase)(PBP5). - <i>Bacillus Subtilis</i> . | 1 | -CAT | TTA~ | 52 | 537 | Reverse |
| 393. | Na ⁺ and Cl ⁻ -dependent gamma-aminobutyric acid transporter homolog-Haemophilus | 1 | TTG | TGA | 2 | 268 | Forward |

| | | | | | | | |
|------|---|---|------|------|-----|-----|---------|
| | influenzae (strain Rd KW20) | | | | | | |
| 394. | Unknown | 2 | ATG | TGA | 319 | 546 | Forward |
| 395. | dihydrolipoamide dehydrogenase (EC 1.8.1.4) - Pelobacter carbinolicus | 1 | ATG | TGA | 3 | 284 | Forward |
| 396. | Unknown | 2 | ATG | TGA | 241 | 450 | Forward |
| 397. | Beta-Glucosidase A (EC 3.2.1.21)(Gentiobiase)(Cellobiase)(Beta-D-Glucoside Glucohydrolase). - Clostridium Thermocellum. | 1 | ATG | TAA | 184 | 453 | Forward |
| 398. | Uracil Permease. - Bacillus Caldolyticus. | 1 | ATG | TAA | 93 | 353 | Forward |
| 399. | Unknown | 2 | ATG | TAG | 127 | 516 | Forward |
| 400. | ligoendopeptidase F- Lactococcus lactis | 1 | ATG | TGA | 134 | 310 | Forward |
| 401. | Stratpasea NCBI gi: 153565NCBI gi: 4- Streptococcus Faecalis DNA. | 2 | ATG | TAA | 392 | 568 | Forward |
| 402. | Unknown | 2 | ATG | TAA | 376 | 507 | Forward |
| 403. | Exodeoxyribonuclease Small Subunit (EC 3.1.11.6) (Exonuclease VII Small Subunit). - Escherichia Coli. | 2 | -CAT | TCA- | 470 | 682 | Reverse |
| 404. | ATP-Depenent DNA Helicase RECG (EC 3.6.1.-). - Escherichia Coli. | 1 | ATG | TGA | 3 | 455 | Forward |

| SEQ ID NO: | Identity | ORF # | Codon | | Position | | Direction |
|------------|--|-------|-------|------|----------|------|-----------|
| | | | Start | Stop | Start | Stop | |
| 405. | Possible thiamin biosynthetic enzyme | 1 | -CAT | TTA- | 15 | 347 | Reverse |
| 406. | SPOU Protein. - Escherichia Coli. | 2 | ATG | TAA | 322 | 618 | Forward |
| 407. | Malonyl Coa-Acyl Carrier Protein Transacylase (EC 2.3.1.39). - Escherichia Coli. | 1 | ATG | TAG | 85 | 498 | Forward |
| 408. | Unknown | 1 | -CAT | CTA- | 17 | 118 | Reverse |
| 409. | nucleoside diphosphate kinase (ndk) homolog- Haemophilus influenzae (strain Rd KW20) | 1 | CTG | TGA | 1 | 159 | Forward |
| 410. | Nucleoside Diphosphate Kinase (EC 2.7.4.6)(NDK) (NDP Kinase). - Escherichia Co LI. | 2 | ATG | TAG | 215 | 481 | Forward |
| 411. | Unknown | 1 | -CAT | TTA- | 21 | 368 | Reverse |
| 412. | Unknown | 2 | -CAT | TCA- | 162 | 314 | Reverse |
| 413. | Unknown | 1 | ATG | TAA | 187 | 417 | Forward |
| 414. | Unknown | 2 | ATG | TGA | 316 | 417 | Forward |
| 415. | Unknown | 1 | ATG | TGA | 316 | 453 | Forward |
| 416. | Enolase (EC 4.2.1.11)(2-Phosphoglycerate Dehydratase)(2-Phospho-DOGlycerate Hydro-Lvase). - Bacillus Subtilis. | 1 | -CAT | TTA- | 4 | 435 | Reverse |
| 417. | Unknown | 1 | CTG | TGA | 1 | 363 | Forward |
| 418. | Unknown | 1 | ATG | TGA | 39 | 383 | Forward |
| 419. | PILB Protein. - Neisseria Gonorrhoeae. | 1 | -CAT | TTA- | 145 | 327 | Reverse |
| 420. | Unknown | 2 | ATG | TGA | 285 | 533 | Forward |
| 421. | Unknown | 1 | CTG | TAG | 2 | 379 | Forward |
| 422. | integrase/recombinase (xprB) homolog - Haemophilus influenzae (strain Rd KW20) | 1 | ATG | TAA | 305 | 421 | Forward |
| 423. | Unknown | 1 | -CAT | CTA- | 173 | 436 | Reverse |
| 424. | Unknown | 1 | -CAT | CTA- | 182 | 427 | Reverse |
| 425. | Unknown | 1 | ATG | TAA | 49 | 372 | Forward |
| 426. | *Mutator Mutt Protein (7 | 1 | -CAT | CTA- | 21 | 446 | Reverse |
| 427. | Unknown | 1 | ATG | TGA | 177 | 380 | Forward |
| 428. | Possible phosphatase | 1 | ATG | TAG | 112 | 402 | Forward |
| 429. | Unknown | 1 | ATG | TGA | 110 | 271 | Forward |
| 430. | Phosphoenolpyruvate Carboxylase (EC 4.1.1.31). - Corynebacterium Glutamicum. | 2 | ATG | TGA | 337 | 561 | Forward |
| 431. | Unknown | 1 | ATG | TGA | 214 | 324 | Forward |
| 432. | 50S Ribosomal Protein L31. - Bacillus | 1 | ATG | TAA | 142 | 426 | Forward |

| | | | | | | | |
|------|--|---|------|------|-----|-----|---------|
| | Subtilis. | | | | | | |
| 433. | glycosyl transferase (IgtD) homolog - Haemophilus influenzae (strain Rd KW20) | 1 | ATG | TGA | 127 | 399 | Forward |
| 434. | Unknown | 2 | -CAT | CTA- | 244 | 435 | Reverse |
| 435. | Unknown | 2 | ATG | TGA | 118 | 309 | Forward |
| 436. | Factor essential for Expression of Methicillin Resistance. - Staphylococcus Aur Eus. | 2 | -CAT | TTA- | 168 | 434 | Reverse |
| 437. | Unknown | 1 | -CAT | TCA- | 2 | 214 | Reverse |
| 438. | Unknown | 1 | TTG | TAA | 2 | 142 | Forward |
| 439. | Unknown | 1 | ATG | TAA | 30 | 191 | Forward |

| SEQ ID NO: | Identity | ORF # | Codon | | Position | | Direction |
|------------|--|-------|-------|------|----------|------|-----------|
| | | | Start | Stop | Start | Stop | |
| 440. | Aspartate Aminotransferase (EC 2.6.1.1) (Transaminase A)(ASPAT). - Bacillus SP. (STRAIN YM-2). | 1 | -CAT | TCA- | 63 | 416 | Reverse |
| 441. | Unknown | 1 | ATG | TAA | 52 | 342 | Forward |
| 442. | Unknown | 2 | -CAT | TCA- | 210 | 455 | Reverse |
| 443. | Unknown | 1 | TTG | TGA | 2 | 517 | Forward |
| 444. | ATP-Dependent DNA Helicase RECG (EC 3.6.1.-) - Escherichia Coli. | 1 | ATG | TGA | 83 | 376 | Forward |
| 445. | Unknown | 1 | ATG | TAA | 70 | 384 | Forward |
| 446. | Cell Division Protein FTSA. - Bacillus Subtilis. | 1 | TTG | TAA | 3 | 371 | Forward |
| 447. | Unknown | 1 | ATG | TAG | 70 | 441 | Forward |
| 448. | Unknown | 1 | ATG | TAG | 104 | 454 | Forward |
| 449. | Unknown | 1 | CTG | TAA | 1 | 159 | Forward |
| 450. | Unknown | 1 | ATG | TAA | 120 | 347 | Forward |
| 451. | Unknown | 1 | ATG | TGA | 31 | 423 | Forward |
| 452. | Unknown | 2 | ATG | TGA | 225 | 416 | Forward |
| 453. | Unknown | 1 | ATG | TGA | 290 | 418 | Forward |
| 454. | Unknown | 1 | ATG | TGA | 3 | 269 | Forward |
| 455. | JAG Protein (SPOIIIJ Associated Protein). - Bacillus Subtilis. | 1 | ATG | TGA | 93 | 365 | Forward |
| 456. | "DNA -3-Methyladenine Glycosidase I (EC 3.2.2.20)(3-Methyladenine-DNA Glycosylas E I | 1 | ATG | TAG | 91 | 282 | Forward |
| 457. | "Glucan I | 1 | -CAT | TTA- | 4 | 150 | Reverse |
| 458. | Unknown | 1 | -CAT | CTA- | 245 | 400 | Reverse |
| 459. | Glutamate/Aspartate Transport ATP- Binding Protein GLTL. - Escherichia Coli. | 1 | -CAT | TCA- | 81 | 218 | Reverse |
| 460. | Unknown | 1 | -CAT | TTA- | 103 | 492 | Reverse |
| 461. | Unknown | 1 | ATG | TGA | 305 | 484 | Forward |
| 462. | Unknown | 1 | -CAT | TCA- | 29 | 355 | Reverse |
| 463. | Unknown | 2 | -CAT | TTA- | 572 | 838 | Reverse |
| 464. | Unknown | 2 | -CAT | TCA- | 652 | 1026 | Reverse |
| 465. | Unknown | 2 | -CAT | TTA- | 318 | 764 | Reverse |
| 466. | Unknown | 2 | ATG | TGA | 719 | 805 | Forward |
| 467. | Llcpyrda NCBI gi: 511014 - Lactococcus lactis. | 1 | ATG | TGA | 134 | 472 | Forward |

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|------|--|---|------|------|-----|------|---------|
| 468. | Unknown | 1 | ATG | TGA | 385 | 492 | Forward |
| 469. | Unknown | 2 | ATG | TAA | 587 | 721 | Forward |
| 470. | galE protein - <i>Neisseria meningitidis</i> | 1 | -CAT | TCA- | 23 | 460 | Reverse |
| 471. | Unknown | 2 | -CAG | TTA- | 717 | 1319 | Reverse |
| 472. | Naphthoate Synthase (EC 4.1.3.36) (Dihydroxynaphthoic Acid Synthetase)(Dhna Sy Nthetase). - <i>Escherichia Coli</i> . | 1 | ATG | TGA | 97 | 414 | Forward |

| SEQ ID NO: | Identity | ORF # | Codon | | Position | | Direction |
|------------|---|-------|-------|------|----------|------|-----------|
| | | | Start | Stop | Start | Stop | |
| 473. | Unknown | 1 | CTG | TGA | 1 | 246 | Forward |
| 474. | Unknown | 1 | -CAT | TCA- | 341 | 748 | Reverse |
| 475. | Unknown | 1 | -CAT | TTA- | 217 | 858 | Reverse |
| 476. | Unknown | 1 | -CAT | TTA- | 499 | 729 | Reverse |
| 477. | Multiple Sugar-Binding Transport ATP-Binding Protein MSMK. - Streptococcus MUTA NS. | 2 | ATG | TAA | 407 | 571 | Forward |

Table 2 shows the correlation between the SEQ ID NO of each DNA sequence of the invention with the SEQ ID NO(S) of polypeptide or polypeptides that its open reading frame(s) encodes. For example, the DNA of SEQ ID NO:1 encodes one polypeptide, that of SEQ ID NO:224. Whereas, the DNA of SEQ ID NO:2 encodes two polypeptides, the polypeptides of SEQ ID NO:225 and SEQ ID NO:226.

TABLE 2

| DNA | Protein (open reading frame) |
|-----|------------------------------|
| 1 | 224 |
| 2 | 225,226 |
| 3 | 227 |
| 4 | 228,229,230 |
| 5 | 231 |
| 6 | 232 |
| 7 | 233 |
| 8 | 234 |
| 9 | 235 |
| 10 | 236 |
| 11 | 237 |
| 12 | 238 |
| 13 | 239 |
| 14 | 240 |
| 15 | 241 |
| 16 | 242 |
| 17 | 243,244 |
| 18 | 245 |
| 19 | 246 |
| 20 | 247,248 |
| 21 | 249,250 |
| 22 | 251 |
| 23 | 252 |
| 24 | 253,254 |
| 25 | 255,256 |
| 26 | 257 |
| 27 | 258 |
| 28 | 259 |
| 29 | 260,261 |
| 30 | 262 |

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| 31 | 263 |
| 32 | 264 |
| 33 | 265 |
| 34 | 266 |
| 35 | 267 |
| 36 | 268,269 |
| 37 | 270 |
| 38 | 271 |
| 39 | 272 |
| 40 | 273 |
| 41 | 274 |
| 42 | 275 |
| 43 | 276 |
| 44 | 277 |
| 45 | 278 |
| 46 | 279 |
| 47 | 280 |
| 48 | 281 |
| 49 | 282 |
| 50 | 283 |
| 51 | 284 |
| 52 | 285,286 |
| 53 | 287 |
| 54 | 288,289 |
| 55 | 290 |
| 56 | 291 |
| 57 | 292 |
| 58 | 293 |
| 59 | 294,295 |
| 60 | 296,297 |
| 61 | 298,299 |
| 62 | 300 |
| 63 | 301 |
| 64 | 302,303 |
| 65 | 304,305 |
| 66 | 306 |
| 67 | 307 |
| 68 | 308 |
| 69 | 309 |
| 70 | 310 |
| 71 | 311 |
| 72 | 312,313 |

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| 73 | 314 |
| 74 | 315,316,317 |
| 75 | 318 |
| 76 | 319,320 |
| 77 | 321 |
| 78 | 322,323 |
| 79 | 324,325,326,327 |
| 80 | 328 |
| 81 | 329 |
| 82 | 330 |
| 83 | 331 |
| 84 | 332 |
| 85 | 333,334 |
| 86 | 335 |
| 87 | 336 |
| 88 | 337 |
| 89 | 338 |
| 90 | 339 |
| 91 | 340 |
| 92 | 341 |
| 93 | 342 |
| 94 | 343 |
| 95 | 344,345 |
| 96 | 346 |
| 97 | 347 |
| 98 | 348 |
| 99 | 349 |
| 100 | 350 |
| 101 | 351 |
| 102 | 352 |
| 103 | 353 |
| 104 | 354 |
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| 115 | 365 |
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| 122 | 372 |
| 123 | 373 |
| 124 | 374 |
| 125 | 375 |
| 126 | 376 |
| 127 | 377 |
| 128 | 378 |
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| 130 | 380 |
| 131 | 381 |
| 132 | 382 |
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| 136 | 386 |
| 137 | 387 |
| 138 | 388 |
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| 140 | 390 |
| 141 | 391 |
| 142 | 392 |
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| 146 | 396 |
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| 154 | 404 |
| 155 | 405 |
| 156 | 406 |

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| 157 | 407 |
| 158 | 408 |
| 159 | 409,410 |
| 160 | 411 |
| 161 | 412 |
| 162 | 413 |
| 163 | 414 |
| 164 | 415 |
| 165 | 416 |
| 166 | 417 |
| 167 | 418 |
| 168 | 419 |
| 169 | 420 |
| 170 | 421 |
| 171 | 422 |
| 172 | 423 |
| 173 | 424 |
| 174 | 425 |
| 175 | 426 |
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| 181 | 432 |
| 182 | 433 |
| 183 | 434 |
| 184 | 435 |
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| 189 | 440 |
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| 197 | 448 |
| 198 | 449 |

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| 199 | 450 |
| 200 | 451 |
| 201 | 452 |
| 202 | 453 |
| 203 | 454 |
| 204 | 455 |
| 205 | 456 |
| 206 | 457 |
| 207 | 458 |
| 208 | 459 |
| 209 | 460 |
| 210 | 461 |
| 211 | 462,463 |
| 212 | 464 |
| 213 | 465 |
| 214 | 466 |
| 215 | 467 |
| 216 | 468,469 |
| 217 | 470,471 |
| 218 | 472 |
| 219 | 473 |
| 220 | 474 |
| 221 | 475 |
| 222 | 476 |
| 223 | 477 |

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Black, Michael

Hodgson, John

Knowles, David

Nicholas, Richard

Stodola, Robert

(ii) TITLE OF THE INVENTION: Novel Compounds

(iii) NUMBER OF SEQUENCES: 477

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation

(B) STREET: 709 Swedeland Road

(C) CITY: King of Prussia

(D) STATE: PA

(E) COUNTRY: USA

(F) ZIP: 19406-0939

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 01-APR-1997

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/014690

(B) FILING DATE: 02-APR-1996

PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/025788

(B) FILING DATE: 22-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gimmi, Edward R

(B) REGISTRATION NUMBER: 38,891

(C) REFERENCE/DOCKET NUMBER: P50466

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 610-270-4478

(B) TELEFAX: 610-270-5090

(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 683 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|---|-----|
| CTCAAACATG GTCTCTTCTA GTTGCATGGT CGCAATCGGA TCCAAGGCTG AGGCTGGGCT | 60 |
| CATCCATTAA GAGGATATCT GGCTTAACAG AGATGGCACG AGCGATACAG AGACGTTGTT | 120 |
| GCTGACCACC TGATAAGGTC AAGGCTGACT TGTGGAGATC GTCTTTAACC TGATCCCAA | 180 |
| GGGCAGCCTG ACTAAGGGAG GTTTCTACGA TTTCATCTAG GACTTGCTTA TCCTTAACTC | 240 |
| CAGCACGTTT ATGCGCAAAG GTAATATTAC GGTAAATTGA CTTAGCAAAT GGATTGGGGC | 300 |
| GTTGAAAAAC CATTCCAATG TGTTTACGCA TTTCATAAAC GTTGATTCTT GGACGGTTGA | 360 |
| CATCAATTCC ACGATAGAGA ATCTGCCAGC TTAATTTAGC AATATCAATG GTATCATTCA | 420 |
| TGCGATTGAG ACTGCGTAAG TAGGTAGATT TCCCGGATCC CGACGGACCA ATCAAAGCTG | 480 |
| TAATTTTATT TCCTTTTCAA TTGCATATCA ATCCCTTAA TGGATTGATT TTTACCATAG | 540 |
| TAAACATGGA CATCCTTAGT AGAAAGGGCT ACTTTTCTT CAGGAAAGGT AAGGATATGC | 600 |
| TTCTCATCCC AGTTATATGT TGACATGGCT TCTCCTTAG GCACGGGTTA ATTTCTTGTC | 660 |
| TAGATAGCTT CCGAACTTAC GAG | 683 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1512 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|------|
| CTAGTCCAAC | TAACTGAGTT | TTCCTTTATC | TATTATATCA | AATATAAGTC | CGTTTGTAACT | 60 |
| TAGTGAAGAA | TTCTTTTGTC | CGCTCTTCTT | TAGGGGTGTG | GATAATCTCA | TCCGGAGTTC | 120 |
| CAGACTCGAT | GATTTTCCCC | TTATCTAAGA | AGAGAATTTT | ATCCGCAACT | TGGGCTACAA | 180 |
| AGGGCATGTC | ATGACTGACC | AAAATCATGG | TCTGACCTGA | CTTAGCAGCA | TCTGCAATAG | 240 |
| ACTTTTCTAC | TTCACCGACC | AATTCTGGGT | CAAGGGCTGA | AGTTGGTTTCG | TCTAAGAGCA | 300 |
| AAACATCTGG | TTTCATAGCA | AGCGCACGCG | CTAGGGCAAC | CCGTTGCTTC | TGTCCACCTG | 360 |
| ATAAATGGCG | AGGATAATGG | TTTTCACGGT | CCGAAAGCCC | AACCTTAGCC | AACTCTTCCT | 420 |
| TGGCAATCTT | AGTCGCTTCT | TGGTCAGATA | ATTTCTTGAC | AACAACCAAG | CCTTCTTTCA | 480 |
| CATTATCAAG | TGCTGTTTCG | CGTTCAAATA | AATTAAACTG | TTGGAAAACC | ATAGACAAC | 540 |
| TACGGCGTAG | GGCAAGGATT | TCTTCTTGAG | TGATTTTAGA | AAAATCAACT | GAAAAACCAT | 600 |
| CAATCTGAAT | AGAGCCACTG | TCAGGTGTTT | CAAGATAATT | GAGACTGCGA | AGAAAGGTTG | 660 |
| ATTTTCCAGC | TCCTGAAGAA | CCAATCAAGG | CTACAACCTC | CCCTTTTGA | ATATCCAAGT | 720 |
| TCAGATGATC | CAAGACAGTC | TGTCCTGAAA | AGGATTTGCT | TAAATTCGAA | ATCTTAATCA | 780 |
| TTAACGAAGG | TCTCCTTTCA | CATCTGTTTG | CACTGTATCA | GGTGCAGAAA | TAGCCATTTT | 840 |
| TCTCTCGATG | AAACGACCGA | GGCTTTCAAT | TCCGATATTG | ACTACCCAAT | AAACAAGGGC | 900 |
| AACAGAGATG | AAGCGTTCAA | AATAGCGATA | ATCAGCTCCA | CCTAGAATCT | GAGCTTGGGC | 960 |
| AAAGACTTCC | ACAACACCCG | CACTAAAAGC | TAGAGATGTT | CCCTTGGTCA | AACCGATGAG | 1020 |
| GGAATTAATC | AAGGTTGGAG | TAGCTACCAC | CGCTGCATTA | GGAATAATCA | CTCGTCGATA | 1080 |
| AACTTGCGCT | CGGGTCATAC | CCAGACTGCG | CGCCGCCTCA | ATCTCACCAG | GATTAACCTGA | 1140 |
| GAGAATGGCT | GCACGAATGG | TTTCACTAGC | ATAAGCTGCC | TCATTAAAGG | CAAAAGCGAC | 1200 |
| AATCGCAAAA | GCTGCAGCTG | GAATCGCATT | GATATTGAGA | CCAGTTCCCC | ATTGCTGATT | 1260 |
| GAGGGCTTTC | AAAGCCAAAG | GGATTCCGTA | GTAGGTCAAC | ATGAGTTGCA | CCAAAATCGG | 1320 |
| TGTCCCTTTT | AAGAACTAA | CAAAGAAGGC | CTGCAAGGGA | TATAAAATCT | TGACACGATT | 1380 |
| GATCTTCACA | ATGGCAAAAA | GAAGCGCCAA | AACCAAGCCA | AAAAGGGCAC | CGCCAATTGT | 1440 |
| CAACATAATT | GTTGTTGGAA | GTTGTTGGAC | AATTCTAGGG | ATTCCATCAA | AGACCGAACG | 1500 |
| TAGGCTAAAC | AG | | | | | 1512 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGGAGATTA | TTGAGATTGC | CCGTCAAAAC | GATTTGATTA | TNITTGCGGA | TGAAATCTAT | 60 |
| GACCGCATGG | TAAATGGACG | GACATGTGCA | TAACGCCTGT | GGCGAGCTTG | GCACCAGATG | 120 |
| TCTTCTGTGT | CAGCATGAAT | GGTCTGTCAA | AATCCCACCG | CATAGCAGGT | TTCCCGTGTG | 180 |
| GGATGGATGG | TCTTGTCTGG | CCCTAAGACT | CATGTTAAGG | GCTATATCGA | AGGGCTCAAT | 240 |

| | | | | | | |
|-------------|------------|------------|-------------|------------|------------|-----|
| ATGCTGTCCA | ATATGCGCCT | TTGCTCTAAC | GTTTGTGGCTA | CCAACGCTGC | ATTAGGAATA | 300 |
| ATCACTGTCTG | TACAAACTTG | CGCTTGGGGG | GTCACCAATC | AGTCGATGAA | TTGCTTCTTC | 360 |
| CTGGTGGACG | AATCTACGAG | CAAAGAAATT | TCATCTATAA | TGCCATTCAA | GATATTCCAG | 420 |
| GTTTGTCTGC | CGTTAAACCC | AAGGCGGGGC | TCTATATCTT | CCCAAAAATC | GACCGCAATA | 480 |
| TGTACCGTAT | CGATGATGAT | GAGCAGTTTG | TCCTTGATTT | CTTGAAGCAG | GAAAAGGTTT | 540 |
| TCTTGGTTCA | TGGTCGAGGC | TTTAACTGGC | AGGAACCAGA | CCACTTCCGT | ATCGTTTACC | 600 |
| TTCTCTGTGT | TGATGAGTTA | GCCCAAATCC | AAGAAAAGAT | GACTCGTTTC | TTGAAACAGT | 660 |
| ATCGTAGATA | GGGCTTGCAT | TCGAAAAAGC | TGGAAACATT | TGCCTAGAG | | 709 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|------|
| CTGCTTCAGA | ACCTGCCAAA | CCAGCACCGA | TAACATTGAT | ATAAGATTGA | GACACGACAC | 60 |
| TAATACCTCT | TTGGGAGTGT | GAAGTTAAGA | TTACATTGA | AAAAGCCAAT | CAGACTTACA | 120 |
| AGCTTTCGAG | TTTCTTGGCT | CAGGCTGAAA | AAGTCCACAG | GGCTTTTNCA | CTCCACAAA | 180 |
| TCTTTCTATT | TTTTCTNCTA | CTAGTATAAC | AAAAAAAGGG | AAGAAGNAA | ACTTCCCTGT | 240 |
| TTAGTCATTT | TCTTGATGTA | AAGAGATAGT | GAGTATTCCA | GTTAAGAATC | AATTATATGC | 300 |
| TACTCTATAA | AATCTTTTCC | ACATAACGGA | TCGATAGGGA | CTGTTATTCT | ATCTCTTGCT | 360 |
| ATAACCGTAT | TATCTAAAAC | AGCATAACAT | TCAACATAGT | GATCTCCTTT | AAACTGTGAA | 420 |
| TCTTCCGTGA | TATTTTATTT | TACCTGAAAA | AATAGCACAC | GCTCACAATT | CTTCCTAATA | 480 |
| GCCTCAGCTT | CAATATTTCT | TACTTTCCAA | TAGACTCCCT | GCGAAACAAA | ATATGGTATA | 540 |
| GTAGTTCTAT | GAATGATGAA | GCAAGTAAAC | AACTAACTGA | TGCACGATTT | AAGCGTCTTG | 600 |
| TTGGTGTTCA | GCGCACGACT | TTTGAAGAGA | TATTAGCTGT | ATTAAAAACA | GCTTATCAAC | 660 |
| TTAAACACGC | AAAAGGTGGA | CGAAAACCTA | AATTAAGCCT | AGAAGACCTT | CTTATGGCCA | 720 |
| CTCTTCAATA | TGTGCGAGAA | TATCGAACTT | ATGAACAAAT | TGCGGCTGAT | TTTGGTATCC | 780 |
| ACGAAAGCAA | CTTAATCCGT | CGGAGCCAAT | GGGTGAAAGT | AACTCTTGTT | CAAAGTGGTG | 840 |
| TTACGATTTT | AAGAACTCCT | CTCAGTTCTG | AGGACACGGT | AATGATTGAT | GCGACGGAAG | 900 |
| TACAAATCAA | TCGCCCTAAA | AAAAGAATTA | GCGAATCATT | CTGGTAAAAA | GAAATTTTAC | 960 |
| GCTATGAAGG | CTCAAGCGAT | TGTCACAAAGT | CAAGGGAGAA | TTGTTTCTTT | GGATATCGCT | 1020 |
| GTGAACATA | GTCATGATAT | GAAGTTGTTT | AAAATGAGTT | GCAGAAATAT | CGGACAAGCT | 1080 |
| GGAAAAATCT | TGGCTGATAG | TGCTTATCAA | GGGCCCATGA | AGATATATCC | TCAAGCACAA | 1140 |
| ACTCCACGTA | AATCCAGCAA | ACTCAAGCCG | CTAATAGCTG | AAGATAAAGC | TTATAACCAT | 1200 |
| GCGCTATCCA | AGGAGAGAAG | CAAGGTTGAG | AACATCTTTG | CCAAAGTAAA | AACGTTTAAA | 1260 |
| ATGTTTTCAA | CAACCTATCG | AAATCATCGT | AAACGCTTCG | GATTACGAAT | GAATTTGATT | 1320 |
| GCTGGCATT | TCAATTATGA | ACTAGGATTC | TAGTTTTGCA | GGAAGTCTAT | TATTTTCCTT | 1380 |

| | |
|---|------|
| ATTGTCTGTA AGTCTACTGA CCTTGTTGTT TATCCCAGTC ATGTTTCTA GTTCGGGCTC | 1440 |
| AGAGTTTCAA AGTGGATGGC AAGAGCATCA ATTGATTGCT GAGAAGGTTA GTAAACACT | 1500 |
| TGACAAGACA TTTGATAAGG ATGTCAGAAA AATTCCGACC AGTCCAGTTT TATCAAAAAT | 1560 |
| TTGTAGATGA GATGGGAAGG ATTTACTC | 1588 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|--|-----|
| CTGTTTTTAA TACAGCTAAC ATCTCTTCAA AAGTGGTACG CTGAACACCA ACAAGACGCT | 60 |
| TAAATCGTGC ATCAGTTAGT TGTTTACTTG CTTTCATCATT CATAGAACTA CTATACCATA | 120 |
| TTTTGTTTCG CAGGGAGTCT AATATTGTCA AATACTGGAG CGCTCATTGC TGGTATACGG | 180 |
| AATAAGATTG GCCCAGCTTC GATAACTGGG ATACCTGGTT CAAAACCAAG ATCTGTTGCA | 240 |
| GCGATTGGTG TAAAGATATC GTAACCTTTC ATAAGGTCTT CGTTTACATC TTTCACCATG | 300 |
| ACTGCATCAC AGTGAACATC ATAACCACGG TTTGAAAGTT CTTCTTCTAG AGCACTTTTA | 360 |
| ATTTGGTGAC TTGAGTTAAC ACCTGCACCG CAGGCAGCAA GAATTTTAAT CATTAGATT | 420 |
| TCCTCCGATT TTATTTTTTA ATAGACAAGA TTAAGCGGTT GCTTCAGCAA TGTAAGCATA | 480 |
| AAGTTTTTCT GGTTCGGAAA TTTTGTATAG GTCTTCAAGA TGTCCATTTC CTGTGAAAAA | 540 |
| GTCCATCAAC TGAGCCAGAA TATTTGTTTG ACTTGAACCT GAGTTATTGA TGATAAGAA | 600 |
| GAGCAAGGAT ACTTCTACTT CCTTATCAGG AGCTATCATA TTGTGAAAAG TTAGTGATTT | 660 |
| TTCTAATCGA ACAACCACCA CTTTTCTCAG | 690 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | |
|---|-----|
| ACTGCTACCT TTAAGAAGAT AGTAGACGTA TATACTTTTT TAAGAAAATC AAAAAGATAC | 60 |
| TATAAAAAAT CTATTTGTTT ATTGAATTGA AGACTTTGGT AACAAATTGA AAATAAAAAG | 120 |

| | |
|---|-----|
| GAGGTATTCA TCATGAATAC AAAAATGATG TCACAATTTT CTGTTATGGA TAATGAAATG | 180 |
| CTTGCTTGCG TTGAAGGTGG AGATATTGAT TGGGGAAGAG AAATTAGTTG TGCAGCAGGG | 240 |
| GTTGCATATG GCGCAATTGA TGGGTGTGCA ACAACGGTTT GATATTTCTA TTGGGACCAT | 300 |
| TTGCTATAGG AATAGGTGTA ACTGGTGCTG CAGGTGGAG | 339 |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|--|------|
| CTGAAGACCT CGTGCTACTC CTCCTCCAAC ACCTGCTTTG GCAAAATCTC CCCAATTGCA | 60 |
| TCCGCCACCT TCAACTCAAG CAAGCATCTC AGTATCCATA ATTTCAAATT GTGACATCTT | 120 |
| TTTGTTATTC ATAACGAATA CCTCTTTTTT ATTTTAAATA TTTGTCTTGT TACAAACTTG | 180 |
| ACAAGTTTAG TATAACAGTA TCTATTAATT TTTTTCATCC AAATCTTGAA TTGGCATCGA | 240 |
| AACGTCTTGA ATTAGCTTTT TTGTTTCAAA ATCATCTCTA TTTTAAAAA AGATGTTTTC | 300 |
| TAATCACTTT TTTACTATTT AGACTTCCTG CAAACTAGA ATCCTAGTTC ATGATTGATA | 360 |
| ATACCAGCAA TCAAATTCAT TCGTAATCCG AAGCGTTTAC GATGATTTG ATAGGTTGTT | 420 |
| GAAAACATTT TAAACGTTTT TACTTTGGCA AAGATATTCT CAACCTTGCT TCTCTCCTTA | 480 |
| GATAGCGCAT GATTACAGGC TTTATCTTCA ACTGTTAGCG GCTTGAGTTT GCTGGATTTA | 540 |
| CGTGGAAGTT TGTGCTTGAG GATATATCTT CATGAGCCCT TGATAACCAC TGTCAGCCAA | 600 |
| GATTTTACCA GCTTGTCGGA TATTTCTCAT TTCTAAAAAC CATCTACTTC CGTTGACTTG | 660 |
| GAATCCGAT TGCTATTTTC CTTGAATGAT TTTAACCACA TCTCCTACAC TTTGGAGTTG | 720 |
| GTCAATTTCC TCATCGCTGA TTTGATACT AAATTCATCC TCCAGCGTCA AGATAAACTC | 780 |
| CATCAAATCA ACTGAGTCAG CATCCAAGTC GTCTTTCAGA CTCAAGGATT CTGTCACGAC | 840 |
| AAAGTCCTCT CCCTGTCGCT CTGGGATAAT GGTCAACAATA CTGTCAAAAA TTTCCTTTTC | 900 |
| TCTCATCTCT TTTATTCTCC TGAAAATTCA CGCGCAGTCT GGGCAACTAC TTCTGTTTCT | 960 |
| AGCATGGTAC GAATCTGGCG AATCGTACTA TAAACAGCCT TGGCATCGCT TGAGCCATGA | 1020 |
| GTCTTGACAA CAGGTGCCTT GACACCAAAC AAGACCGCTC CACCAACATC TGAATAATTG | 1080 |
| AGCTGTTTTT TCAAACCTCT GAGGCTGTCC TTGAGAAAGG GGGCACCTAG TTTCGCTCGA | 1140 |
| AGACCACCAC CTGTAATAGC TGTCTTGAGC AAGCCCATGA TTCCCATAGC TGTCCCTTCG | 1200 |
| ATGGATTTGA GCACAGCGTT TCCCGTGAAA CCATCTGCCA CAACAACATC TGCAACGCCA | 1260 |
| TTTCATCAAAT CACGCGCTTC CACGTTTCCG ATAAAGTTCA AACTTTCATC AGCCGCCAGT | 1320 |
| AATTCATAAG TTTCTTACG AAGCGGGTCG CCCTTGCTAC TCTCTGTTCC GTTGTGAGC | 1380 |
| AAACCAACAC GTGGTTGCGC AATGCCACGA ACATTCTTGG CATAGAAAGA ACCTAGGACA | 1440 |
| GCGTATTGAT GGAGGTGCTG GGCTGTATTT TCTGCATTAG CACCGAGGTC AAGCATGTCA | 1500 |
| AAACCTTTCC CATCTACAGT CGGCAATGTT GACATAAGTC CAGGACGGTC GATATTCTTG | 1560 |
| ATACGACCCA CGATGAAGAA TCCAGCAGCC AACAAAGCAC CTGTATTCCC AGCCGAAAGG | 1620 |

ACAGCGTCTG CTTCAACCATC TTTGACAGCC TTGGCTGCCA ATACCATACT GGCATTTTTC 1680
 TTATTCCGAA TAG 1693

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAAATCTGC TTGCTTAGTC CACTTGCTTG AGCCAAGGAG TCACATACTC AAAATTTTCA 60
 TGAAAGTCAT AGGTACCGTC TTCTTTTSTA GCTGAAAAGA AAAGTCCATC GTGGTAGAGC 120
 AAATCCCCGT GGGCCATAAT TCTGGCAGTT TTTTCCTCTT CCTACTCCTG AGACTTTTGC 180
 TTAGTCCCCT CTTGAGAAAT AGTATCTCGT TTTTGACTAG TCAAGGGATT CCTTGAAGC 240
 TTTCAAACAA CAAGACCAAG CCCATTGATA AACCAACTGC TAGCAAGAGT ATCGCCACAA 300
 ATCCCTTATT GCTCCACTTG CGATAACTCC TAAAAAGTTT ACCAAGCCCT TCATAAAACG 360
 AAAAGCTAAA CCACCCTGAT TTCGATTTTG TCTTCTTTGT ATCTTCGTTT TCCCTACTTT 420
 CTTATGCAAG CCTTTTCTTT TTATTATATC ACAGATAAGT ATTTCTTTCA CAATTGAATT 480
 GAACCTCCCA TCTATTTTCT ATAAATCCTA AATGCCATAA TGCTTTCAAT TCCTGTCATT 540
 TTGTGATATC ATGTAGAAGA AATGAACATA TCCACAGTGG CTTATTCCAA GTATACCACT 600
 TGGGCTTTGG CAGTAG 616

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1973 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAATATAGA ATAATCACCG CCGTTGTGAA AGAACGATTG GATGATAATC CAATCGTTCA 60
 GGGAAATTGG AAGACCTTGG GTTCCAATT TAGGCATGAG ACACCTTTGG TGGCTGCTGC 120
 CGTCCCTCAC AAGCTAAGGT GATTGTTGAA AAAGAGGAAA AAGGAGAAGA AATGAAACCA 180
 GTAATTCCA TCATCATGGG CTCAAAATCC GACTGGGCAA CCATGCAAAA AACAGCAGAA 240
 GTCCTAGACC GCTTCGGTGT AGCCTACGAA AAGAAAGTTG TTCCGCACA CCGTACACCA 300

| | | | | | | |
|------------|------------|------------|-------------|-------------|------------|------|
| GACCTCATGT | TCAAACATGC | AGAAGAAGCC | CGTAGTCGTG | GCATCAAGAT | CATCATCGCA | 360 |
| GGTGCTGGTG | GCGCAGCGCA | TTTGCCAGGC | ATGGTAGCTG | CCAAAACAAC | CCTTCCAGTC | 420 |
| ATTGGTGTGC | CAGTCAAGTC | TCGTGCTCTT | AGTGGAGTGG | ATTCACCTCTA | TTCTATCGTT | 480 |
| CAGATGCCGG | GTGGGGTGCC | TGTTGCGACC | ATGGCTATCG | GTGAACTCTT | TTTTAGGATA | 540 |
| TAAACAGGG | TTCCGATAAG | TTTTTTTGCA | AGGTGGATGA | TGGCTACATT | GTAATGTTTT | 600 |
| CCTTATTCTA | ACTTAGTCTT | AAGATAGGTC | TTAAAACCAG | GTGAAAACCG | AAGGCATGCT | 660 |
| TTGGCAGCTT | GTATGAGTAC | CTACCGCAGA | TGAAGGGAAC | CCCGTTTGAC | CATCCTTCCA | 720 |
| ACTAAATCAA | TCTGACCTGA | CTGATAAATA | GAAGAATCCA | GTCCAGCGAA | AGCTTGTAAT | 780 |
| TGAGCAGGAT | TATCAAAGGC | ATGAATATTT | CGAATCTCGG | CTAAAATGAC | CGCCCCTAAA | 840 |
| CGATTCTCAA | TCCCAGTAAC | CGTCGTGATG | ACCGAGTTTA | ACTCAGCCAT | CAAGTCATTG | 900 |
| ACACATTTTT | CCGCCTTGTC | AATGAGCCTC | TTGTAATGTT | TGATGTTTTT | ATTACACGAG | 960 |
| ATAAACGTC | TATGCGTTAT | CAAACTCATT | ACCAATTAAA | ACAAATGTGG | TTAGATCCTT | 1020 |
| TCGGAATTG | TCAAGCGATT | GGAGGAAATG | AACATAATCCA | CAGCGGCTTA | TTCCAAGTAT | 1080 |
| ACCACTTGGG | CTTTGGCAGT | AGCTAACTGC | GCTAAATATA | ATATAAGGAG | GAGTAAATG | 1140 |
| AAGACAGTTC | AATTTTTTTG | GCATTATTTT | AAGGTCTACA | AGTTCTCATT | TGTAGTTGTC | 1200 |
| ATCCTGATGA | TTGTTCTGGC | GACTTTTGCC | CAAGCCCTCT | TTCCAGTCTA | TTCTGGACAA | 1260 |
| GCGGTGACGC | AGCTAGCCAA | TTTAGTTCAA | GCTTATCAAA | ATGGGCAATC | CAGAACTTGT | 1320 |
| ATGGCAAAGC | CTATCAGGAA | TTTATGGTCA | ATCTTGGCCT | GCTGGTTTTG | GGTCTATTTT | 1380 |
| ATCTCTAGGT | GTAATATAAA | CATGTGTCTC | ATGACGCGCG | TGATTGCAGA | ATCGACCAAC | 1440 |
| GAGATGCGCA | AAGGTCTCTT | TGGTAAGCTT | GCTCAGTTGA | CGGTTTCTTT | CTTTGACCGT | 1500 |
| CGACAAGATG | GCGATATCCT | GTCTCATTTT | ACCAGTGATT | TGGATAATAT | CCTCCAAGCC | 1560 |
| TTTAACGAAA | GCTTGATTCA | GGTCATGAGC | AATATTGTTT | TATACATTGG | TCTGATTCTT | 1620 |
| GTCATGTTTT | CGAGAAATGT | GACGCTGGCT | CTCATCACCA | TTGCCAGCAC | CCCATTGGCT | 1680 |
| TTCTTATGCT | TGATTTTCAT | CGTGAAAATG | GCACGTAAAT | ACACCAACCT | CCAGCAGAAA | 1740 |
| GAGGTAGGGA | AGCTCAACGC | CTATATGGAT | GAGAGCATCT | CAGGCCAAAA | AGCCGTGATT | 1800 |
| GTGCTAGGAA | TTCAAGAGGA | TATGATGGCA | GGATTCTTG | AACAAAATGA | GCGCGTGCGC | 1860 |
| AAGGCAACCT | TTAAAGGAAG | AATGTTCTCA | GGAATTCTTT | TCCCTGTGAT | GAATGGGATG | 1920 |
| AGCCTGATTA | ATACAGCCAT | CGTCATCTTT | GCTGGTTCGG | CTGTACTTTT | GAA | 1973 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTAAACCAAT | AGTTGCTGAA | GACCATAATC | CAGCTGCTGT | TGTTAAACCT | TTAACTTTTT | 60 |
| GATTAGTTAC | CATGATTGTT | CCTGCCCTTA | GGAAACCCAA | GCCACTAATT | ACTTGGGCTC | 120 |
| CCATTGACT | AGGATCACCG | CTACCATAAC | GACTAGTGAT | GAAGTATTTT | GTCATCATTA | 180 |

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|------|
| CAACACAAGT | TCCCAAACAA | ACTAGTAAGT | AGGTTCTAAT | CCCTGCTGCT | TGGTTTTTGA | 240 |
| CTCCTCGCTC | ATAGCCAACA | ATGCCACCGA | AAAGAATCGC | TAAAAAGCAC | CTAAGAAGTA | 300 |
| TTTCCCAAAT | ACTCAGTTCG | TATGAAAGAT | TCATATTATC | TCTTACCTCG | TTTACCTTGG | 360 |
| AATAGGCTTG | ATAAATAAAG | AGCTGCACTA | GACATAATCA | TTAAAATTAC | AGAATAAACA | 420 |
| AACATCATTG | CCTGTGCATT | TAAAGTTGCT | GTTTCATCAG | TAGACTGTTT | AATAACGATT | 480 |
| CCCAATGGTT | GGAAAAGTGG | ATGGTACAAG | AATACAGATA | AGTCATAGTC | AGATAATAAA | 540 |
| GAATTAAAGT | TTAACACAAC | TACTGATAAT | ACGACTGGTA | AAATATACGG | TATAATAACT | 600 |
| CGCACCATAG | TGTAGAAACT | AGATGCACCC | ATACTACGTG | CAGCTTCTTC | CATATCATT | 660 |
| TCTATACTGA | AAAATACAGC | CCGAATCATT | CTATAAGAAA | ATGGTAATTT | TTGAATAGTA | 720 |
| TATGCAATAA | GTAAATAAAT | TACTGTTCCCT | ACTAAACTA | AATTAAATAG | TATTAAATGA | 780 |
| GGTATATTAT | AAGTGAACAT | TAATCCTAGT | GCAATCAATG | TACCTGGCAA | TATCCATGGT | 840 |
| ATCAGTGCAC | CATACTCAAA | GAATTTATCG | AACTTACTCT | TGTTTTTATG | TACAATACGT | 900 |
| GAAATTACTA | TTGCTATAAT | TGTAGCAATT | ACCGCAGCTA | AAATTGCATA | AACAACGCTG | 960 |
| ACTAGGTAAG | GACGAAATGA | TTGAGCATCT | GTAAATAAAT | TAGCATAGTT | CGCTAACGTA | 1020 |
| AATTTAGATA | GATCTAAAGT | TCCCGTCTTG | ATCGTCAACG | AGTCTGTAAA | CGAGTATAGA | 1080 |
| ATTATCAAAA | CTATTGGTAA | CATATAGATT | GCAAACAATA | CATACGCAGC | AATGTGAGCA | 1140 |
| AGAATTATTC | CATAATGGAG | AAGAAAATTA | TCTGCTTCCT | TAATACTAGC | CTGGTTTTTCG | 1200 |
| AAACAGAAAT | | | | | | 1209 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CTAAGTCCTT | TTAGTTTTAT | CTTAATTCTC | TTATTGTTGT | AATAATCAAT | ATAGTCTATA | 60 |
| ATGGCTTGTT | CCAATTGCTT | AAGCGACTGA | AACGACTTCT | CATAACCGTA | AAACATTTC | 120 |
| GATTTCAGAA | TCCCAAAGAA | AGATTCCATC | ATACCGTTGT | CTTGGCTGTT | TCCCTTGCGT | 180 |
| GACATAGATG | CTTGAATTCC | CTTACTCTTA | GGAACCGATG | ATAAGAATCG | TGTTGGTATT | 240 |
| GCCAGCCTTG | GTCACATATG | AGAATCGTAT | TCTCGTAGTG | CTTCTCTGTG | AATGCCTGTT | 300 |
| CCAACATTGT | TTGTACTTGT | TCTAAGTTGG | GTGAAGTTGA | AAGATTATAG | GCGATAATTT | 360 |
| CGCTATTAAA | GCCATCTAAA | ACTGGTGATA | AGTAAAGCTT | TTGAGTACTT | GCTGGAATGG | 420 |
| CAAATTCTGT | CACATCTGTG | TAGCACTTTT | CCATTGTTTT | AGAGCCTTCA | AATTGGCCTT | 480 |
| GAATGAGATT | CTCTGCCTTC | TTACCAACGT | CTCCTTTATG | AGAAGATTTC | GTTTCTGTCTG | 540 |
| CATTTTAGCT | TGTAAATTGA | GTAATTTTCA | CAAGCCTTGA | ACTCTTTTAT | GATTTACCAG | 600 |
| ATAAGCACGA | TTCCTTAGTT | CTAAATGAAT | ACAGCGATAA | GCATAATTTC | CCTTGTGTTT | 660 |
| GATAAAAATG | GATTGAATTT | CAGCTTTAAG | CTCTTGGTCC | TTATCTGGTT | TGNTAG | 717 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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CTAAATCACC AGATTTAACC AAGTCGTAGA TACGGCCTGG TGTTCCAATA ACAATATGAG      60
GCTGATTGCT TGCCAATTTT TCAATCTGGC GAGCCTTATC CGTACCACCC ACATAATTAA      120
CCACACGAAC TTCGACATCT GAGTGAGCTG AAATCTGACG CGCTACTTGG TAAATTTGAG      180
TAGCCAACTC ACGACTCGGT GCAGTAATCA CTGCTTGTA ACTATCGCTA GCTTCATCTA      240
ATTGCTGGAA AATCGGTAAC AAGAAAGTAT GAGTCTTACC TGAACCTGTT TTTGATTCTC      300
CTACTAGGTC ACGACCTGCC AAAACAATAG GAATCAACTT GTCTTGACCC TCTGTTGGAG      360
TTGTAAATTT TAACTCCTCC AAGGCTTCTC TAATATAGTT TTTAAATTGA AATTCGTAA      420
ATGACATAAC ATCCTCGATT CTATCTATCT TATCAATTAT ACCATATTTT ATTCCATTAC      480
AGTAGTCTCA CTTATTTAGG CTATTTCCAG TAGCTTCTCT AGTAAGAAAA GGCTGGAATT      540
TTATAGTTC AACCTCTTTT CAGTTATTAT TTCCAGTTTA ACATAGCATT CAAGCCATAG      600
TGATCACTCA CTTGTGGACT CTTGTTACCA TCAAATACGA CATGTAAATT TTCCACCGCT      660
AACTCTTTGG TAGTAAAGAC ATAATCGATT CGAAGGGGTT CAGTGTTCCT TTTCCAGCCA      720
TCAATTCAG GCGGAACAGT ATAGCTACCA CTTTCTCTTT GAGCAACTTC AAATGCGTCT      780
TGTAAGCCTA ATGGACTAGC TAAATAGCT TGTAACCTT CCCTGACCTG CTGGGTTGTT      840
AAAATCTCCA G

```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

CTGTTGAGAT TGTTACGAAA TAACTGAAAA TATTTAAGGA GAAAATATAT GTTGAAACAC      60
TTAAACTTAA AAGGTCACCT ATTGACAGCC ATTTCTTATA TGATTCCAAT TGTTTGTGGT      120
GCAGGATCTC TAGTTGCCAT TGGTTTAGCA ATGGGGGGTG GTGTTCTCTG CGCTCTTGTA      180
GCAGGAAAAT TCACTATCTG GGATGCTTTA GCAACTATGG GTGGTAAAGC CCTTGGTCTC      240

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| | |
|--|-----|
| TTGCCAGTTG TTATTGCTAC AGGTTTGTCT TACTCGATTG CTGGTAAGCC AGGGATTGCA | 300 |
| CCAGGTTTGT TTGTTGGTCT AATTGCCAAT TCTGTTGGTT CAGGGTTTAT CGGTGGTATC | 360 |
| TTGGGAGGTT ATATAGTTGG TTTCTTGGTT CAAGCGATTA TTA AAAAGGT CAAAGTACCA | 420 |
| AAGTGGATTA AAGGTTTAAT GCCAACCTTG ATTATTCCTT TTGTACCTCT TTGGTAAGTA | 480 |
| GTTTGATTAT GATTATATT ATTGGGGCGC CTATCGCAGC CTTTACCAAC TGGTTGACGA | 540 |
| G | 541 |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | |
|---|------|
| CTGGAATGAG TGTATAAGCC CAGCCCAAGT TTTGCATCCG TTCAAAGTTC CAAGACCCTT | 60 |
| GTAAGAAGGT TGAACGCCAC CAAACTTTTT TACGATCTGA TTAGTTAAT TGAAGTTTTT | 120 |
| CAGTCATGAT GTTTTCAGTC CTTTCTTATC TTAGTAGTCT TCTAGGATAT CGCCGATTGG | 180 |
| GTCGTTAGAA GTTGCGGCTC CTCCGCCACC ATTTCCACCA GTTTTAGAAA GGTGAAGGTA | 240 |
| GATAAGAGCG ATAGCAACAC CGATAGCACC GAATCCGATT AGAGTAATAT CTGACACAGC | 300 |
| AGCGAGAACG AAACCAAGAG CGAAGAATGG CCATACTTCA CGAGTTGCCA TCATGTTGAT | 360 |
| AACCATGGCG TAACCAACGG CAACGACCAT ACCACCACCG ATAGCCATAC CATCTTTGAG | 420 |
| CCAGTCTGGC ATGGCACTAA GGATACTTTG TACAGTTTCA GTTGGTACCA TAAGGAGAAG | 480 |
| AGCTGCAGGA AGCGCGATAC GAAGTCCTTG GAAAAGTAGC GCAATGAAAT GCGCACGCTC | 540 |
| CACAGCGCCG AAGTCACCTT TTTTAGCGGC AGCATCTGCA GTATGAACCA AACCAACTGA | 600 |
| AATTGTACGA ACAATCATTG TCAAGAAAAG TCCAGCTACG GCAAGAGGGA TAGCAACCGC | 660 |
| TTGGGCAACA CCGATACCAG TCTTGGTAAA GTCACCACCA AGAACCATGA TAATGGCAGC | 720 |
| AGCGACAGAA GCAAGTGACG CATCAGGAGC GATAGCAGCA CCGATATTTG ACCAACCAAG | 780 |
| GGCAATCATT TGAAGCGATC CACCGAGGAT AATCCCTGCT TCCAAGTGGA CCTGTTACAA | 840 |
| GCCCAATAAG GGTACAGGCT ACAAGTGGTT GGTGAAATTG GAACTGGTCG AGGATGCCTT | 900 |
| CAAGACCTGC AAAGGAAGGC TACAACGACT ACTAAAACCA TAGAAATAAT AGACATGTTT | 960 |
| AAAATCCTTT CATAAATAAT GGCTTATTTG ACATTGGCTT TGTTAATCAA GTCAAACAAA | 1020 |
| TCTTTTTTAG AATCATTTGG TACTTTACCG ACATCAAATT CAACACCCAA GTCACGCATT | 1080 |
| TTTTCAAATG TAGCAACATC TTCTTTGTCC ATAGACAAAA CGGTATTGAC CAATGTTTTA | 1140 |
| CCTGTTGAGT GAGCCATAGA ACCAACGTTA AGAGTCTTGA TTGGCAGGCC GCCTTCGATG | 1200 |
| GCACGAAGGG CATCTTGAGG TGTTTCAAAC AAGATAAGGG CATGTGTTTC TCCAAAACGT | 1260 |
| GGGTCTTTTG AAATATCAAT CAGTTTTTGA ATTGGAACCA CGTTAGCCTT GACATTACCT | 1320 |
| GGAG | 1324 |

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

TCATAAGGAA GCTGTCGCTC GTTCCGCTAA GGTATGGACA CCACGGTGAA CATTGGCATT      60
GTCCTGCTCA TAGTAAGTGT TAATAGCTTT CAGAACTACT AGTGGTTTMT GTGTCGTCGC      120
AGCATTGTCC AGATAGACCA GAGGTTCATC ATTGACAATC TGATCTAAAA TTGAAAATC      180
CTTGCGAATC GCTTCTACAT CTAACATAGG CTTCCCCTTA GCGTTTTGAC AATTCTCTTT      240
CGATAGTTGC AATCATTTC A TCACGAACTT CTTGACTGG AATCTCCACG ATAACAGATC      300
CAAGGAAACC ACGAACAACC AAACGCTCTG CAGTTGCCTT ATCCAATCCA CGACTCATGA      360
GGTAATACAT GTCTTCTGGA TCAACTTGTC CGATAGACGC TGCCTGTCCT GCAGTGACAT      420
CATTTTCATC AATCAAAAGA ATTGGGTTAG CATCTGAACG CGCTTGGTCT GAAAGCATGA      480
GAACACGGCT CTCTTGTTGC GCATCTGCTC CCTTAGCACC CTTGATGATG TGGCCGATAC      540
CATTGAAAGT CAAAGTTGCT TTTTCAAGGA TAACCCCATG TTGTAGGATA TTTCCGATAG      600
AGTTGCAGCC ATAGTTAGTT ACACGAGTAT CAATCCCTTG TACCTGACGA CCACTTGAAA      660
GAG                                                                 663

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

CTAGTTGGAT GGCTTCAATA AAGGATGATT TGGCTGCTCC ACTATTGGCA ATGAGCTGAA      60
AACAGATATA TTCCATTCTT TCGTCATCTT ATTTCTCCTA TCCATTCAAG TGCTTGTTCC      120
AGAACTTTTG CTCCATTTCAT CATTCCGTAA TCCCGCATAT CAATGGTATC TACAGGGATA      180
TTTCCTGCAA TTTCTTTCAC AGCAAGTAAC TCATAACGAA TTTGTGGCCC AATTAGAATG      240
ACATCTGCTT CATGGATATT CTTTTAGCT TCTGTCATTG ATTTTGCTTG GATAGAAATT      300
TCAATCCAC GTTCACTGCG ACTTTGTTGC ATTTTTTTAA CAAGCATACT TGTGACATT      360
CCCGCATTAC ATACTAATAA AATTTGTTT ATAATCTTAA CCTTCCATTT CTTGTTCAAC      420
AACTTTGTCA TTAACCTTGA TAAATGGAAT GTATAGAAGA ACTCCAAGTG CAAAGATGAT      480

```

| | |
|--|-----|
| GAATTGAACT AGAACTGCTC TCACGTCCCC TGCTGTTGCT AACCATGCAT TTAAGAATAC | 540 |
| TGGTGTAAGTC CAAGGAACTT GTATAAATGC AGGACTCATG AATCCTGTAA CTGTTGCTAA | 600 |
| GTAGCTGATT AAAATACCAA GGACTGGAAC TGTGATAAAT GGAATAGTC | 649 |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | |
|---|-----|
| CTTGGTATTA TTTGAAATCA GATGGTTCTT ATGCAAAAAA TGCATGGCAA GGAGCTTATT | 60 |
| ACCTTAAATC AAACGGTAAA ATGGTACAAG GTGAGTGGGT TTATGATTCT TCTTACCAAG | 120 |
| CCATGGTATT ACTTGAAATC AGATGGTTCA TATGCTCGCA ATGCATGGCA AGGAAACTAC | 180 |
| TATTTGAAAT CAGATGGTAA AATGGCTGTC AATGAATGGG TTTATGATGC CACCTATCAA | 240 |
| GCATGGTATT ATTTGACATC AGATGGTTCT TATGCTTACA GTACATGGCA AGGAAATTAC | 300 |
| TATCCTAAAA TCGGATGGTA AAATGGCTGT CAATGAATGG GTTGATGGTG GACGTTATTA | 360 |
| TGTTGGCGCT GACGGAGTTT GGAAGGAAGG TCAAGCAAGT ACAGCTTCTC CTAGTAATGA | 420 |
| TAGCAATAGT GAATATTCCT GCTGCTTTAG GAAAGGCAAA AAGTTATAAT TCGTTATTCC | 480 |
| ACATGTCAAA AAAAACG | 497 |

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

| | |
|---|-----|
| CTAGTCTAAA TTTTTTAAAA CAAAGGTCAA AGATAGTCAA TATCAGTAAT CATAACTAAG | 60 |
| TAAACAAAAA GAGGTAAAGA ATATGAATAA CAACTTTAAT AATTTTAATA ACATGGATGA | 120 |
| TTTATTTAAC CAATTGATGG GTGGTATGCG AGGATACAGT TCTGAAAATC GCCGTTACTT | 180 |
| AATTAATGGA CGCGAAGTCA CACCTGAGGA ATTTGCTCAC TATCGTACGA CTGGTCAATT | 240 |
| ACCAGGAAAT GCAGAACTG ATGTGCAAAT GCCACAACAG GCATCAGGTA TGAAACAAGA | 300 |
| CGGTGTCCTT GCAAACTAG GTCGAACTT GACAGCAGAA GCGCGTGAGG GCAAGTTGGA | 360 |

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|------|
| TCCTGTTATC | GGACGAAACA | AGGAAATTCA | AGAAACATCT | GAAATCCTCT | CACGCCGCAC | 420 |
| CAAGAACAAAT | CCTGTTTTGG | TCGGAGATGC | AGGTGTTGGT | AAGACAGCAG | TTGTCTGAAGG | 480 |
| TCTAGCGCAA | GCCATTGTGA | ACGGAGATGT | TCCTGCTGCT | ATCAAGAACA | AGGAAATTAT | 540 |
| TTCTATTGAT | ATCTCAGGTC | TTGAGGCTGG | TACTCAATAC | CGTGGTAGCT | TTGAAGAAAA | 600 |
| TGTCCAAAAC | TTAGTCAATG | AAGTGAAAGA | AGCAGGGAAT | ATTATCCTCT | TCTTTGATGA | 660 |
| AATTCACCAA | ATTCTTGGTG | CTGGTAGCAC | TTGTGGAGAC | AGTGGTTCTA | AAGGGCTTGC | 720 |
| GGATATTCTC | AGCCAATCGA | TCTCTCTCGT | GGAGAATTGA | CAGTGATTGG | GGCAACAAC | 780 |
| CAAGACGAAT | ACCGTAACAC | CATCTTGAAG | AATGCTGCTC | TTGCTCGTCG | TTTCAACGAA | 840 |
| GTGAAGGTCA | ATGCTCCTTC | AGCAGAGAAT | ACTTTTAAAA | TTCTTCAAGG | CATTTCGTGAC | 900 |
| CTCTATCAAC | AACACCACAA | TGTCATCTTG | CCAGACGAAG | TCTTGAAAGC | AGCGGTGGAT | 960 |
| TATTCTGTTT | AATACATTCC | TCAACGTAGC | TTGCCAGATA | AGGCTATTGA | CCTTGTCGAT | 1020 |
| GTAACGGCTG | CTCACTTGGC | GGCTCAACAT | CCAGTAACAG | ATGTGCATGC | TGTTGAACGA | 1080 |
| GAAATCGAAA | CGGAAAAAGA | CAAGCAAGAA | AAAGCAGTTG | AAGCAGAAGA | TTTGAAGCA | 1140 |
| GCTCTAAACT | ATAAACACG | CATTGCAGAA | TTGGAAGGA | AAATCGAAAA | CCACACAGAA | 1200 |
| GATATGAAAG | TGACTGCAAG | TGTCAACGAT | GTGGCTGAAT | CTGTGGAACG | AATGACAGGT | 1260 |
| ATCCCAGTAT | CGCAAATGGG | AG | | | | 1282 |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTTGATATAA | TTCTTGTTTC | GAAAGATTCT | CCTTAGGTAT | ATCTATTCCT | CCACTAGTAA | 60 |
| ACGGTAATTC | CAAAACAGAG | TTTACTTCGT | TAAATGTAAG | CCAATATTTA | ACTTTATCTT | 120 |
| TATACCTTTC | TAAACGTGT | CGAGCAAATT | TTTCATAAAA | ATGAATCATT | CTTCCTATCA | 180 |
| ATCCATCCAT | GATATTTTCT | TGCTAAATAT | AATGGAGTCT | CATAGTGTGA | AAGAGTTACA | 240 |
| AGTGGTTCTA | TCCCGTGAGC | ATGTAGTTCA | TCAAACAATT | CATCATAATA | TTTCAATCCA | 300 |
| GCTTCGTTAG | GTTCTTCCTC | ATCTCCTTTT | GGAAAAATTC | TACTCCATGC | AATAGAAGTA | 360 |
| CGAAAAACAT | TAAAGCCCAT | TTCAGAAAAC | AAGGATATAT | CTTCCTTATA | TTTATGATAA | 420 |
| AAATCAATAC | CTATCAATTT | TAAGTTATCT | TCTGTAGGAT | TTTCTGTTGC | TTCTCCTAAT | 480 |
| CCACCTTTGG | GTAACACATC | CTGAACGAT | AAGCCCTTAC | CATCTTCATT | ATATGCTCCC | 540 |
| TCTACTTGAT | TAGCTGCAAC | AGCTCCACCC | CAAAGAAAAT | CATCTGGAAA | AATGGTCATA | 600 |
| ACTTTCCTCC | ATTATAATAT | TACCAGTAAT | TCCTTAGAAA | TGCTCGATTG | TCTGATTATT | 660 |
| AGGTAATATT | AATACATCTA | GAAAATCATT | GGTATTCGTT | ACAATTACTG | GTGTAACGTG | 720 |
| TTCGTAGCCT | TTAGTCTTGA | TTAAATTCAA | GTCCATTTC | AAAATCAACT | GATTTTTGAA | 780 |
| AACTCTGTCT | CCTTCTTCTA | CATGACTAAT | AAAACCTTGA | CCTTTTAG | | 828 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

AGCTATGGTC AGACTCAGAT TGATGGCGTT GCTTATGCCA AGTACGATAT CTTCCGTTTA      60
AAGAACGGGA AAATTGTGGA GCATTGGGAT AATAAGGAAG TCATGCCTAA GGTAGAAGAC      120
TTGACCAATC GAGGGAAGTT TTAAATTGAG GACAAAGAAT GATTGAATAC AAAAATGTAG      180
CACTGCGCTA CACAGAAAAG GATGTCTTGA GAGATGTCAA CTTACAGATT GAGGATGGGG      240
AATTTATGGT TTAGTAGGG CCTTCTGGGT CAGGTAAGAC GACCATGCTC AAGATGATTA      300
ACCGTCTTTT GGAACCAACT GATGGAAATA TTTATATGGA TGGGAAGCGC ATCAAAGACT      360
ATGATGAGCG TGAACCTCGT CTTTCTACTG GTTATGTTTT ACAGGCTATT GCTCTTTTTC      420
CAAATCTAAC AGTTGCGGAA AATATTGCTC TCATTCTGA AATGAAGGGG TGGAGCAAGG      480
AAGAAATTAC GAAGAAAACA GAAGAACTTT TGGCTAAGGT TGGTTTACCA GTAGCCGAGT      540
ATGGGCATCG CTTACCTAGT GAATTATCTG GTGGAGAACA GCAACGGGTC GGTATTGTCC      600
GAGCTATGAT TGGTCAGCCC AAGATTTTCC TCATGGATGA ACCCTTTTCG GCCTTGGATG      660
CTATTTTCGAG AAAACAGTTG CAGGTTCTGA CAAAAGAATT GCATAAAGAG TTTGGGATGA      720
CAACGATTTT TGTAACCCAT GATACGGATG AAGCCTTGAA GTTGGCGGAC CGTATTGCTG      780
TCTTGCAGGA TGGAGAAATT CGCCAGGTAG CGAATCCCGA GACAATTTTA AAAGTGCCTG      840
CAACAGACTT TGTAGCAGAC TTGTTTGGAG GTAGTGTTC TACTAATTT AATTGCAACT      900
TTTCAGGATC GTTTTAGTGA TTGGTTGACA GCTACAATGA CATTGGTCGG TTCCTTGAGC      960
AAGAGATAGA TTAGCCAGAC AGTCATGCCC AAAATCCCTC CAGGTAAGAG CATAGACCGT     1020
TGCACATTAA GTACGATTAA AAAAGTGATA ATGGCAAGAA AACTTGCTAC TGCTTGTAAT     1080
AAAAAGGTTG TTAGTGTCTAT ATTAGTTCAT CAATACCAAG GCGACAGAAG TTCCTGCCCC     1140
TAAAGCGAGG GTAATGAGCA GGGATTCAAA CATCTTACTC ATACCAGAGT TTATGTGGTT     1200
GGTCATAATA TCACGGACCG CATTGGTCAA GGCAATACCT GGTACAAACG GCATGACCGC     1260
ACCAGCTATA ATCAAATCCT GCCCCTTTGA ATGGAAAAAC CCTGTGTTAG CCGAGCCCCA     1320
AAACTGGGGC CAATTTATCC CCCAAAGACA AAAGCTCCAT CAAAGGCTGT CACAAAGGGA     1380
ATTCGGATAA ATTTTCCACA TAGAAGGAAA AGGCAAAACC AAATAAGGTC GCCACTCCTG     1440
CCCCAAGTGC TCGTAAATAT TCCGCT

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

AAGGTTCTTC GTAAATGTAC ACCATTCGGA TGCTCAAAAT GGGTTCTGAA GCTGCTGCTA    60
AATCTGCACA AGAACACGGT CTTAAATCAG TTGAAGTTAC TGTAAAAGGT CCAGGTTCTG    120
GTCGTGAGTC AGCTATTTTCG TCGCTTGCT GCCGCTGGTC TTGAAGTAAC AGCAATTCGT    180
GATGGGACTC CAGTGCCAAC ACAATGGTGC TTCGTCCTCC AAAACGTCGC CGTGATAAT    240
CATCGCATT AACTGCTTTT CGTTTAAGAG GGAGTAACTA AATGATCGAG TTTGAAAAAC    300
CAAATATAAC AAAAATTGAT GAAAATAAAG ATTATGGCAA GTTAGTAATC GAACCACTTG    360
AACGTGGCTA CCGTACAGCT CTTGGTAACT CTCTTCGTCG TGTACTTCTA GCTTCTCTAC    420
CAGGAGCAGC TGTGACATCT ATCAACATTG ATGGTGTGTT ACATGAGTTT GACACAGTTC    480
CAGGTGTTTCG TGAAGACGTG ATGCAAATCA TTCTGAACAT TAAAGGAATT GCAGTGAAAT    540
CGTACGTTGA AGACGAAAAA ATCATCGAAC TGGATGTTGA AGGTCCTGCT GAAGTAACAG    600
CTGGTGACAT TTTGACAGAT AGCGATATTG AAATTGTAAA TCCAGATCAT TATCTCTTTA    660
CAATTGGTGA AGGTTCTTCT CTAAAAGCGA CTATGACTGT TAACAGTGGT CGTGGATATG    720
TACCTGCTGA TGAAAATAAA AAGGATAATG CACCAGTTGG AACACTTGCT GTAGATTCTA    780
TTTATACACC AGTTACAAA GTCAACTATC AAGTGAACC TGCTCGTGTA GGTAGCAATG    840
ATGGTTTCGA CAAATTAACC CTTGAAATCT TGACAAATGG AACAATTATT CCAGAAGATG    900
CTTTAGGGCT TTCAGCAGT ATTTTGACAG AACATCTTGA TTTGTTTACA AATCTTACTG    960
AGATTGCTAA GTCAACTGAA GTGATGAAAG AAGCTGATAC TGAATCTGAC GACCGTATTT    1020
TAGATCGTAC GATTGAGGAA CTGGACTTGT CTGTGCGTTC ATACAACTGT TTAAAACGTG    1080
CCGGTATCAA TACTGTGCAT GATTTGACAG AAAAATCTGA AGCAGAGATG ATGAAAGTAC    1140
GAAATCTTGG ACGCAAGAGT TTGGAAGAAG TGAAACTCAA ACTCATTGAT TTGGGTCTTG    1200
GATTAAAGA TAAATAAAGG AGGAATACAT GGCTTACCGT AAACAGGAC GCAC TAG    1257

```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

CTATTGAAC AAGAAAAATA GAGATCRAA GAAAGAGAAC TTATGAATAT TCAAGAAGAA    60
ATTAAGAAAC GTCGTACCTT TGCCATTATC TCCACCCCGG ACGCGGGGAA AACAACCATC    120
ACTGAGCAGT TACTCTAACT TTGGGGGTGA GATTCGTGAG GCTGGTACGG TAAAAGGGAA    180
GAAACAGGG ACTTTTGCTA AATCTGACTG GATGGATATC GAGAAGCAAC GTGGGATTTC    240

```

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| TGTTACTTCA | TCTGTTATGC | AATTTGACTA | CGACGGCAAG | CGCGTGAATA | TCTTAGACAC | 300 |
| GCCAGGGCAC | GAGGACTTCT | CAGAAGATAC | CTATCGTACC | TTGATGGCGG | TGGATGCTGC | 360 |
| GGTCATGGTC | GTGGACTCTG | CCAAGGGGAT | CGAGGCTCAA | ACAAAGAAAT | TGTTTGAGGT | 420 |
| TGTGAAACAT | CGTGGCATTG | CAGTCTTTAC | CTTTATGAAC | AAGTTGGATC | GTGACGGTCG | 480 |
| TGAGCCTTTG | GATCTCTTGC | AAGAATTGGA | AGAAATCTTG | GGCATTGCTA | GCTACCCAT | 540 |
| GAAGTGGCCT | ATCGGGATGG | GGAAAGCCTT | TGAGGGCTTG | TATGACCTCT | ATAACCAACG | 600 |
| TTTAGAGCTT | TACAAAGGGG | ATGAGCGTTT | TGCTAGCCCT | AGAAGATGGA | GACAAACTTT | 660 |
| TTGGTAGCAA | TCCTTTCTAC | GAGCAAGTCA | AGGATGACAT | TGAGCTTTTA | AATGAAGCTG | 720 |
| GGAATGAGTT | TTCAGAGGAA | GCTATTCTGG | CTGGAGAATT | GACGCCTGTC | TTTTTCGGTT | 780 |
| CAGCCCTGAC | AAACTTTGGT | GTGCAGACCT | TCCTTGAAAT | CTTCCTCAAG | TTTGCTCCAG | 840 |
| AACCACATGG | TCACAAGAAA | ACAGACGGTG | AAATTGTGGA | TCCTTATGAC | AAGGATTCTT | 900 |
| CAGGCTTTGT | CTTTAAATC | CAAGCCAACA | TGGATCCTCG | TCACCGTGAC | CGTATTGCCT | 960 |
| TTGTCCGTAT | CGTATCAGGC | GAATTTGAGC | GTGGCATGAG | TGTCAATCTC | CCTCGTACTG | 1020 |
| GTAAGGGTGC | CAAACTATCT | AATGTTACCC | AGTTTATGGC | GGAGAGTCGT | GAGAATGTGA | 1080 |
| CCAATGCCGT | AGCAGGTGAT | ATTATCGGGG | TTTACGATAC | CGGTACTTAT | CAGGTTGGGG | 1140 |
| ATACCTTGAC | GGTTGGAAAA | AACAAGTTTG | AATTTGAACC | ACTGCCAACC | TTTACTCCTG | 1200 |
| AAATTTTCAT | GAAAGTTTCT | GCTAAGAATG | TTATGAAGCA | AAATCCTTC | CACAAGGGGA | 1260 |
| TTGAGCAATT | GGTGCAAGAA | GGAGCCGTTT | AGCTTTATAA | GAATTACCAA | ACAGGTGAGT | 1320 |
| ACATGCTGGG | AG | | | | | 1332 |

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTGGACGCTG | GAACAAATCC | AAGCTGACCT | GTTCCAAGAC | CAGACTTGGT | ATGCTCTGGC | 60 |
| TTATGATGGG | GCAGAAGTGA | TTGGCTTTCT | AGCTGTTTCT | GAGACTCTTC | TTTGAAGCAG | 120 |
| AAGTCCTGCA | AATCGCTGTC | AAAGGAGCCT | ATCAGGGTAA | GGGCATTGCG | TCAGCCTTGT | 180 |
| TTGCTCAATT | GCCGACAGAC | AAGGAAATTT | TCCTCGAAGT | CAGACAGTCA | AATCAACCAG | 240 |
| CGCAAGCATT | TTACAAGAAA | GAAAAGATGG | CAGTTATCGC | TGAGCGAAAG | GCCTACTACC | 300 |
| ATGACCCAGT | CGAGGACGCC | ATTATCATGA | AGAGAGAAAT | AGATGAAGGA | TAGATATATT | 360 |
| TTAGCATTTG | AGACATCCTG | TGATGAGACC | AGTGTGCGCG | TCTTGAAAAA | CGACGATGAG | 420 |
| CTCTTGTTCA | ATGTCATTGC | TAGTCAAATT | GAGAGTCACA | AACGTTTTGG | TGGCGTAGTG | 480 |
| CCCGAAGTAG | CCAGTCGTCA | CCATGTCGAG | GTCATTACAG | CCTGTATCGA | GGAGGCATTG | 540 |
| GCAGAAGCAG | GGATTACCGA | AGAGGACGTG | ACAGCTGTTG | CGGTTACCTA | CGGACCAGGC | 600 |
| TTGGTCGGAG | CCTTGCTAGT | TGGTTTGTCA | GCCGCCAAGG | CCTTTGCTTG | GGCTCACGGA | 660 |
| CTTCCACTGA | TTCTGTAA | TCACATGGCT | GSGCACCTCA | TGGCAGCTCA | GAGTGTGGAG | 720 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCTTTGGAGT | TTCCCTTGCT | AGCCCTTTTA | GTCAGTGGTG | GGCACACAGA | GTTGGTCTAT | 780 |
| GTTTCTGAGG | CTGGCGATTA | CAAGATTGTT | GGAGAGACAC | GAGACGATGC | AGTTGGGGAG | 840 |
| GCTTATGACA | AGGTCGGTCG | TGTCATGGGC | TTGACCTATC | CTGCAGGTCG | TGAGATTGAC | 900 |
| GAGCTGGCTC | NTCTNGGGCA | GGANATTTAT | GA | | | 932 |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | | | | | | |
|-------------|------------|-------------|------------|------------|------------|------|
| CTAAACTTTC | GTCATAGGC | ATACAAATTA | ATCCTTTGGC | ATAAGTAGCC | ATAAAATTAA | 60 |
| CATTTTCTGT | TGTAGCTGCT | TGTGCAGAAC | AAATTAAGTC | TCCTTCATTT | TCTCTATCCT | 120 |
| TGTCGTCTAT | AACAAGAACA | AGTCGTCCCT | TCTGCAATGC | TTCTAATGCT | TCTTGTATTT | 180 |
| TTGATATTC | CATTGACTGA | TTATCCTTTC | TGCTAAAATC | CATTTTGATA | TAATAGTTCC | 240 |
| TTGATATTT | CTGATTTTGG | AGAGTTATCC | ATCAGTTTTT | GCACATATTT | ACCTAAGATA | 300 |
| TCATTTTCAA | GATTTACTGT | ACTCCCGACT | TGTTTACTCT | TAAGAATGGT | TTGTTTCAAG | 360 |
| GTATGAGGGA | TAACAGATAC | TGAAAAGTTT | ACTTTGGAGA | CTTTAGCGAC | AGTCAGACTA | 420 |
| ATGCCGTCAA | TTGTAATAGA | TCCTPTTTCA | ACTATTAAAT | CTAAAATTTT | TTTTTGTGTG | 480 |
| TTGATTTGAT | ACCATACAGC | ATTATCATCT | TTTTTTATMG | ACGAGATTTT | TCCTGTACCA | 540 |
| TCAATGTGTC | CTGTAACGAC | GTGACCCCCA | AGTCGACCGT | TGACAGATAA | GGCTCTTTCT | 600 |
| AGATTCACCT | CACTTCCATG | TTTTAATAGA | GTAAGAGCTG | TTGACTCCA | TGTTTCATTC | 660 |
| ATTACATCAA | CTGTAAAGGA | TTGATGATTG | AAATGAGTAA | CTGTAAGACA | GATACCATTT | 720 |
| ACTGCTATAC | TATCGCCTAA | ATGGATATCC | GTTAATATTT | TTGAGGCTTT | AATTGATAGT | 780 |
| TTACAATTAC | GAGAGTCTTT | CTGTATTCCT | TCAACTTTTC | CGATTTCTTC | AATTATTCCT | 840 |
| GTGAACATGG | ATAAATCACT | TCACCTTTCTA | TGAGATAGTC | NTTTCCTNTT | TGAGAAAAAG | 900 |
| CATAAGGTTT | CAATCTAATA | GCGTCATTTG | GCAAAGAAAT | GCCTTCACCT | CCGACAGGAA | 960 |
| ACTTGGCACT | GCCTCCAAAA | ATTTTGGTG | CAATATATAT | TTTCAGCTCA | TCAACAATTT | 1020 |
| GTTGTTCCAA | AGCACTCCAA | TTCAATTAGAC | TGCCCCCCTC | TACAACTAGG | CTATCAATCT | 1080 |
| GCA TGTTTCC | TTAGATGTTN | GCATTAAACT | CNGATAAGTC | TATATGATTG | CCTTTTTTCT | 1140 |
| TTATGGAAAG | TATTCCCC | | | | | 1158 |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| TAAAGGCTGT | TTGGATAATG | TAACATAAAG | AAATCTTGTT | TAGCAGGGAT | TGAATAGAGT | 60 |
| TCCTGAAGTG | ATGACTTCTT | TATTAGACAT | AATGTCTGGA | CCCAAGATTA | AAAGAATGGC | 120 |
| CCCGAAGAAT | ACGAGCATCA | AAGGTAGCAG | ATGCAACAAC | TGTATCGTGG | AAGATTGAGA | 180 |
| GGAACCTTAGG | TAATTTAAGA | TTGTCTAAAC | TTTCTTCTTT | CTTACCAAAG | CGTCCTGCTA | 240 |
| CTTTATCTAC | AAACCAGATT | GCAAATTGCT | GTGCGTGACC | AATCGCAAAT | CCGCCACCAC | 300 |
| CAGTCAAGCG | TTGAGTTGCC | TCAACAGTCA | TATTTGAACT | AACTGCCCAG | TAAAGTCCAC | 360 |
| AGATGATACC | AATCGCTGCT | GTACCGTAAG | CATTGCGCAA | TTGTGGTACT | AAGAATAGAA | 420 |
| CCATAAGAGA | TACTGTTGCA | GCTAGCCATG | CTGATCAATT | CCCTCAACCA | GTCCTATATC | 480 |
| TCAGCCAAGA | GAATCGAGGA | GGTCTTTGCG | GAATCTCCCG | AAAACATCCA | TTCAGAATTA | 540 |
| GAACAAAAGC | AAGTTACCAG | TGGTCGGGTT | TTACAAGTCC | AAGAATTGAC | TTTTACCTAT | 600 |
| CCTGATGCGG | CCCAGCCTTC | TCTGAGAGAC | ATTTCTTTTG | ATATGACTCA | AGGACAAATC | 660 |
| CTTGGTATCA | TTGGGGGGAC | TGGTCTGGT | AAATCAAGCT | TGGTGCAACT | CTTACTTGGA | 720 |
| CTTTATCCAG | TAGACAAGGG | GAACATTGAC | CTTTATCAAA | ATGGACGTAG | TCCTCTTAAT | 780 |
| TTGGAGCAGT | GGCGGTCTTG | GATTGCCTAT | GTACCTCAAA | AGGTCAAAC | CTTTAAGGGA | 840 |
| ACTATTCGTT | CCAACCTGAC | TTTAGGTTTA | AATCAAGAAG | TATCTGACCA | GAAACTCTGG | 900 |
| CAGGCCTTGG | AGATTGCGCA | AGCTAAGGAT | TTTGTCACTG | AAAAGGAAGG | ACTTTTGGAT | 960 |
| GCCCTAATTG | AAGCAGGGGG | GCGAAATTTC | TCAGGTGGAC | AAAAACAAAG | GTTGTCTATC | 1020 |
| GCCCGAGCAG | TCTTGCGCCA | AGCTCCGTTT | ATCATCCTAG | ATGATGCAAC | CTCGGCACTG | 1080 |
| GATACCATTA | CAGAGTCCAA | GCTCTTGAAA | GCTATTAGAG | AAAATTTTCC | AAACACGAGC | 1140 |
| TTAATTTTGA | TCTCTCAACG | AACCTCAACT | TTACAGATGG | CGGACCAGAT | TCTCCTCTTG | 1200 |
| GAAAAAGGTG | AGTTGCTAGC | TGTTGGCAAG | CACGATGACT | TGATGAAATC | CAGCCAAGTC | 1260 |
| TATCGTGAAA | TCAATGCATC | CCAACATGGA | AAGGAGGACT | AGAATGAAAC | GACAAACTGT | 1320 |
| AAACCAGACG | CTCAAACGTT | TAGCCGTAGA | TTTAGCAAAC | CATCCCTTCC | TCCTTTTCCT | 1380 |
| AGCCTTTCTA | GGAACATTG | CCCAAGTTGG | CTTATCAATT | TACCTACCTA | TTCTGATTGG | 1440 |
| GCAGGTCATT | GACCAAGTCC | TAGTGGCTGG | TTCATCACCA | GT | | 1482 |

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|-----|
| CTCTGAAGGA | TCCAGAAAGT | CGCTTATATA | TTTTATTAAA | AGACGGTCAG | GTTATTGGGA | 60 |
| CTTGTACGGT | TGATTTATCG | ACTAATACGA | ATTACTTCTA | CGGTTTAGCA | ATATTGGAAC | 120 |
| CTGAACGTGG | AAAAGGCTAT | GGAAGCTACT | TAGCAAAATC | CCTCGTCAAC | CAACTAATTG | 180 |
| AGCAAAATGA | CAAGGAATTT | CAGATTGCAG | TGGAAGATAG | CAATGTAGGT | GCCAAACGTT | 240 |
| TGTATGAAAA | AATTGGCTTT | GTCAAACAGA | CTCAGGTGGT | TTATCTGAAT | GAGAAAGGAG | 300 |
| CAAGGGATTC | CGAAGTGTAG | AGATATTCCG | ACTGAAATTT | ACTTGAAC TT | TTAGTGATGA | 360 |
| AACTAATTGT | TCTTGGA TTT | CAGCTTTCCT | GATTATGATT | TATGATTAAA | ATCTATGACA | 420 |
| CCATGTCTCG | TGATTGCGA | GAATTTGTCC | CGATTGAGGA | CGGCAAGATC | AAGATGTATG | 480 |
| TTTGTGGGCC | AACGGTGTAC | AACTATATCC | ACGTGGGAAA | CGCCCGTTCG | ACGGTAGCTT | 540 |
| TTTTGGATAC | GAATTTTCGT | GCTATTTTGA | GTACCGTGGG | TATAAGGTTG | CCTATATTTT | 600 |
| CAATTTTACA | GATGTGGATG | ATAAGATTAT | CAACCGTGCC | AGGGAAGAAG | GCATCACGCC | 660 |
| TCAGGAGGTT | GCGGATAAGT | ACATCGCTGC | CTTTCGTGAG | GATGTGACGG | CCTTGGGCGT | 720 |
| GAAACCTGCG | ACTCGCCATC | CGCGTGTAGT | GGAGTTTATG | GCAGACATCA | TCCGTTTGT | 780 |
| GGAAGACTTG | ATCGAGAAAG | GCTTTGCCTA | TGAGAGTCAA | GGGGATGTCT | ATTTCCTGT | 840 |
| AGAAAAATCC | CACAACTATG | CTAAATTGGC | TAATAAAACC | TTGGAAGATT | TGGAG | 895 |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| CTGTTTGCCC | TTTCTTCTAA | TAAAGAATTG | GCAGAACGTG | TGGCGCAGGA | GATTGGGATA | 60 |
| GAGTTGGGGA | AATCAAGTGT | TCGCCAATTT | TCAGATGGAG | AGATTTCAGGT | CAACATTGAA | 120 |
| GAATCAATCC | GTGGGAAACA | CGTCTTTATC | CTACAATCAA | CTAGTTCGCC | TGTAAATGAC | 180 |
| AATCTGCTTG | AAATTTTGAT | TATGGTAGAT | GCTTTGAAGC | GTGCGAGTGC | AGAATCTGTC | 240 |
| AATGTTGTCA | TGCCTTACTA | TGGGTATGCA | CGTCAGGATA | GAAAGGCGAG | AGCGCGTGAG | 300 |
| CCAATCACTT | CAAACTTGT | CGCAAATATG | CTTGAAGTAG | CTGGAGTGGA | TCGTTTATTG | 360 |
| ACCATCGACT | TGCATGCTGC | GCAAATTCAA | GGATTCCTTG | ATATTCCTGT | GGATCATTTG | 420 |
| ATGGGTGCTC | CTCTGATTGC | AGATTATTTT | GAGCGTCCTG | GTATGGTTGG | TTCTGACTAT | 480 |
| GTGGTTGTCA | GCCCCGACCA | TGGAGGGGTG | ACTCGTGCTC | GTAAGTTGGC | AGAATTTTGT | 540 |
| AAAACATCTA | TCGCTATTAT | TGAGAAACGT | CGTAGCGTTG | ATAAGATGAA | TACTAGTGAA | 600 |
| GTTATGAACA | CCATCGGTAA | GGTTGAAGGC | AACCACTTGT | AGCTTCGATT | GATGATATGT | 660 |
| ATTGATACCG | CTGGAACGAT | TTGTCATGCC | GCAGATGCTC | TTGCGGAAG | | 709 |

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

CTAGAAGAAC TCCGTCACAA GCTTGTGACT TGTAAGCAAG AACAGAGCAA GATTGAGGAT      60
TCCTTATGAT TTCATTCTT CTCTATTGG TCTTGGTTTG GGGATTTTAT ATCGGCTATC      120
GGAGAGGCCT GCTCTTACAG GTTTATTACC TGATTTCAGC CATGGCATCG GCTTTTATGG      180
CTGGCCAGTT TTATAAGGGG CTGGAGAGC AATTCCATTT ATTGCTCCCT TATGCAAATT      240
CGCAGGAAGG TCAGGGGACT TTCTTTTCC CATCGGATCA ACTCTTTCAG CTGGATAAGG      300
TCTTTTATGC AGGTATCGGC TACTTGCTTG TATTTGGGAT TGTCTATAGC ATTGGTCGTT      360
TGCTTGGTCT TCTCTTACAC TTGATTCTTA GCAAAAAACT GGGTGGTAAG TTGTTCCAAG      420
TTTCAGCAGG TATCTTGTC ATGTTGGTGA CCTTATTTGT CTTGCAAATG GCCTTGACAA      480
TCTTGGCGAC CATCCCCATG GCAGTTATAC AAAATCCTCT TGAAAAGAGT ATCGTCGCAA      540
AACACATCAT CCAGAGCATA CCGATAACAA CCAGTTGGCT CAAACAAATC TGGGTGACAA      600
ATTTAATCGG ATAAAAAGGG CAGGAGTTT CCTAGCCCTT TGTTTACAGA TTTGACTCGA      660
ATCTATCAGA ATGTAAAAAG CTACCACACC TAGACATTCA AAGACAAGGA AATAAAGATG      720
AATAAGAAAA TATTAGAAAC ATTAGAGTTC GATAAGGTCA AGGCCTTGTT TGAGCCTCAT      780
TTGTTGACCG AGCAGGGCTT GGAGCAATTG AGACAG      816

```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1001 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

CTTGAAGCAG CTGAAAGCAT GGGGTCTTCG GGATTTAAAA CCTATTCGTA ACGGGTTGTT      60
TTACCTTTCC TAGTTCCAAC CTTACTAGCA GTCCTTGCT TGTATTTATG AGAGCATCTCT      120
CAGACTTTGG AACGCCTATG TTGATTGGCG AAGGATATCG GACTTTCCCT GTCCTGATTT      180
ATACCCAATT TATTAGCGAG GTTGGAGGAA ATTCTGCTTT TGCAATTATG GCGATTATCA      240
TTGCCTTGGC AATTTTCCTT ATCCAAAAAC ACATTGCAAA CCGCTACAGT TTCAGCATGA      300
ATCTGCTCCA TCCAATTGAG CCTAAAAAAA CTACAAAAGG AAAAATGGCT GCCATTTATG      360
CAACAGTCTA CGGAATTATC TTTATCTCTG TTTTACCTCA AATCTACTTA ATTTATACCT      420
CTTTCCTAAA AACATCAGGT ATGGTATTTG TTAAGGTTA TTCTCCAAAC AGTTACAAGG      480

```

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| TAGCTTTCAA | TCGTATGGGA | TCTGCTATTT | TCAATACCAT | TCGTATCCCT | TTGATTGCCT | 540 |
| TAGTTCTAGT | TGTTCTTATT | TACGACATTT | ATCTCCTACC | TAGCCGTTAG | AAAACGGAAT | 600 |
| TTGTTTACAA | ACTTAATTGA | CAGCCTCAGT | ATGGTACCTT | ATATTGTACC | AGGAACCGTT | 660 |
| CTAGGGATTG | CCTTCATTTT | TTCCTTCAAT | ACTGGTCTAT | TTGGAAGTGG | ATTTCTTATG | 720 |
| ATTACAGGGA | CTGCTTTCAT | CTTGATTATG | TCTCTATCTG | TCAGAAGATT | ACCGTATACT | 780 |
| ATTCGCTCAT | CTGTTGCTAG | CTTACAACAA | ATAGCACCAA | GTATTGAAGA | AGCTGCTGGA | 840 |
| AAGCTTAGGA | AGTAGTCGTC | TCAATACCTT | TGCTAAGATT | ACAACTCCAA | TGATGCTATC | 900 |
| TGGTATCATT | TCTGGAGCCA | TCTTATCTTG | GGTCACAATG | ATTTCAAAAC | TCTCTACTTC | 960 |
| TATCCTCCTC | TACAATGTCA | AAACAAGAAC | AATGACTGTA | G | | 1001 |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1064 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|------|
| CTGGTTTGCA | ATCTATTCCA | ACTGAGATTA | CAGAGGCAGC | AAGGATTGAT | GGTGCGACTA | 60 |
| GCAAGCAAGT | TTTCTGGAAC | ATTGAATTGC | CTTACTTGCT | ACCAAGTGTC | TCTATGGTCT | 120 |
| TTATCCTAGC | CCTAAAAGGT | GGGCTGACTG | CCTTTGACCA | AGTCTTTGCC | ATGACCGGTG | 180 |
| GTGGTCCAAA | CAATGCCACA | ACCTCACTTG | GGCTCTTGGT | TTATAACTAT | GCCTTTAAAA | 240 |
| ACAACCAATT | CGGTTATGCC | AATGCCATTG | CCGTAATCTT | GTTCTCTTA | ATTGTAGTGA | 300 |
| TTTCGATCAT | CCAATTGAGA | GTATCTAAGA | AATTTGAAAT | TTAAGAGGAG | AAGCATGATG | 360 |
| AAACAAGATG | AAAGAAAAGC | CCTGATTGGC | AAATACATTC | TATTGATTCT | AGGATCGGTT | 420 |
| CTGATTTTAG | TGCCGCTCCT | TGCTACCCCT | TTTAGTTTCT | TTAAACCCAC | TAAGGATATT | 480 |
| GTAGATAATT | TCTTTGGCTT | TCCAACCAAC | TTCACATGGG | ACAACTTTAG | CCGTCTCTTA | 540 |
| GCTGATGGGA | TTGGAGGCTA | TTATTGGACT | CTGTCGTCAT | CACTGTCTTG | TCTTTACTTG | 600 |
| CAGTAATGAT | CTTTATCCCT | ATGGCAGCCT | ACTCCATCGC | TCGCAATATG | AGTAAAAGAA | 660 |
| AAGCCTTTAC | CATTCATGTA | TACCCCTCTTA | ATCCTCGGAA | TCTTCGTACC | TTTCCAAGTC | 720 |
| ATCATGATTC | CGATTACGGT | TATGATGAGT | AAACTCGGTT | TGGCTAATAC | CTTTGGTTTG | 780 |
| ATCTTGCTCT | ACTTGACCTA | TGCGATTCCA | CAGACCCTCT | TTCTCTATGT | TGGATATATC | 840 |
| AAAATCTCGA | TTCCAGAAAG | TCTGGATGAA | GCAGCAGAGA | TCGATGGGGC | TAATCAATTT | 900 |
| ACAACCTATT | TCCGCATCAT | NTTCCCAATG | ATGAAACCGA | TGCATGCGAC | AACCATGATC | 960 |
| ATCAATGCCC | TTTGGTTCTG | GAATGACTTC | ATGTTGCCAC | TCCTTGCTCT | GAACCGGGAT | 1020 |
| TCCAAAATGT | GGACTCTGCC | TTTGTTCCAA | TACAACTACG | CAGG | | 1064 |

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | |
|---|-----|
| CTGTAAAAGA AGTTAATCAA GTTGATAAAG CACTTTTAAA ACAAATTGGT GCAGTTGATG | 60 |
| TCTTAGAAGT GAAGGGTGGC ATTCAAGCAA TCTATGGAGC AAAAGCAATC TTATATAAAA | 120 |
| ATAGTATTAA TGAAATTTTA GGTGTAGATG ATTAAGTACT TACTGACTTA ATAAAAACA | 180 |
| GAGGAGAGTG ATGGATGAGT AGGATGAAAT GAAATCGCAT ACAAGAAATA AAGAATCAT | 240 |
| TATCCAAGTT GGATACGCTT ATTACATAGG AGAATACAAA TGAAATTTAG AAAATTAGCT | 300 |
| TGTACAGTAC TTGCGGGTGC TGCGGTCTT GGTCTTGCTG CTTGTGGCAA TTCTGGCGGA | 360 |
| AGTAAAGATG CTGCCAAATC AGGTGGTGAC GGTGCCAAAA CAGAAATCAC TTGGTGGGCA | 420 |
| TTCCCAAGTAT TTACCCAAGA AAAAAGTGGT GACGGTGTG GAACTTATGA AAAATCAATC | 480 |
| ATCCAAGCGT TTTGAAAAAG CAACCCAGAT ATAAAGTGA AATTGGAAAC CATCCACTTC | 540 |
| CAGTCCAGTC CTGAAAAATC ACAACAGCCA TCCGAAGCAG GAACAG | 586 |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

| | |
|---|-----|
| TGGTAGTTCT TCCTAGTGCA GGGGCTGTAG ACCCAGTTGC GACCCTAGCG CTGGACTAGT | 60 |
| CGAGAGGGTG TTGTTGAAAA TGGATGGNTA TCGCTATGTT GGTATCTAT CAGGTGACAT | 120 |
| CCTCAAAACG CTTGGCTTGG AACTGTGTTT AGAAGAAACC TCAGCAAAAC CTGGAGAGGT | 180 |
| GACTGTAGTC GAAGTTGAGA CTCCTCAATC AACAACAAAT CAGGAGCAAG CTAGGACAGA | 240 |
| AAACCAAGTA GTAGAGACAG AGGAAGCTCC AAAAGAAGAA GCACCTAAAA CAGAAGAAAG | 300 |
| TCCAAAGGAA GAACCAAAAT CGGAGGTAAA ACCTACTGAC GACACCCTTC CTAAAGTAGA | 360 |
| AGAGGGGAAA GAAGATTCAG CAGAACCATC TCCAGTTGAA GAAGTAGGTG GAGAAGTTGA | 420 |
| GTCAAAACCA GAGGAAAAAG TAGCAGTTAA GCCAGAAAGT CAACCATCAG ACAACCAGC | 480 |
| TGAGGAATCA AAAGTTGAAC CACCAGTAGA ACAAGCAAAA GTCCCAGAAC AACCCGTGCA | 540 |
| ACCTACACAA GCTGAGCAAC CAAGTACACC AAAAGAATCA TCACAACAAG AAAATCCTAA | 600 |
| AGAAGATAGG GGAGCGGAAG AGACACCGAA ACAAGAAGAT GAACAGCCAG CAGAAGCCCC | 660 |
| AAGAAATCAA GGTGAAGAA CCAGTAGAAT CAAAAGAGGA GACTGTTAAT CAACCTGTTG | 720 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| AACAACCAAA | AGTGGAACG | CCTGCTGTAG | AAAAACAAAC | GGAACCAACA | GAGGAACCAA | 780 |
| AAGTTGAAGT | AACAAGTATT | CCCCAACTA | CTCGCTATGA | GGAAGACCTT | ACTAAGGAAC | 840 |
| ACGGAACGCG | TGAAGTTGTT | AAGGAAGGTA | AGAATGGCAG | TAGAACAGTT | ACTACTCCAT | 900 |
| ATATCTTGAA | TGCGACAGAT | GGTACGACTA | CAGAAGGCAC | TTCGACAAC | GATGAAGCTG | 960 |
| AGATGGAGAA | AGAGGTTGTT | CGTGTGGCA | CGAAACCCAA | AGAAAAATTA | GCTCCAGTCT | 1020 |
| TAAGTTTGAC | AAGTGTTACA | GATAATGCAA | TGTTGCGTAG | TGCGAGACTT | ACTTATCATT | 1080 |
| TGGAAAATAC | AGATAGTGTT | GATGTGAAAA | AAATTCATGC | TGAAATTAAA | AATGGCGATA | 1140 |
| AGGTTGTCAA | AACTATTGAC | TTATCTAAAG | AGAGATTATC | AGATGCTGTT | GACGGTCTTG | 1200 |
| AACTTTATAA | AGATTATAAG | ATTGTGACGA | GTATGACCTA | TGATAGAGGT | AATGGTGAAG | 1260 |
| AAACCTCTAC | GTTGGAAGAA | ACTCCACTAC | GATTAGACCT | CAAGAAGGTT | GAATTGAAAA | 1320 |
| ACATCGGCTC | TACTAATCTC | GTCAAAGTAA | ATGAGGATGG | TACTGAGGTG | GCAAGTGACT | 1380 |
| TCTTAACAAG | TAAACCTGTG | GATGTGCAGA | ATTACTACCT | CAAAGTAACT | TCCCGTGATA | 1440 |
| ATAAAGTTGT | TTCCCCTCCC | AGTTGAAAAA | ATTGAAGAGG | TGACTGAGGA | AGGTCCACCA | 1500 |
| CTTTACAAAG | TCCCTGCTAA | GGCCCTAATT | TGAT | | | 1534 |

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| CGGATTTGTT | TATCTCAAGA | AGAGTCGCGA | TATTCTCCGT | GAAAGTTCAG | AATTGATTAN | 60 |
| CCAAACGGTA | GAAGATTATC | TTCAAGGAGA | TGACTTTGAC | TGGGCAGATC | TTAAAGGGAA | 120 |
| GGTTCGANAT | AATTTGACCA | AGTATCTCTT | TGACCAAACC | AAGCGTCGTC | CANCTATTTT | 180 |
| ACCAAGTAGTC | ATGGAAGCAA | AATAATCGTT | GAAATAAACA | GAGAGAAAGT | CGAGTTTCGG | 240 |
| CTTTTCTTA | TAGAAAAATA | GAAGGAGAAA | ATCATGGCAG | TAATGAAAAT | CGAGTATTAC | 300 |
| TCACAAGTAT | TGGATATGGA | GTGGGGGGTG | AATGTCCTCT | ACCCTGATGC | CAATCGAGTG | 360 |
| GAAGAACCAG | AGTGTGAAGA | TATTCCTGTC | TTGTACCTTT | TGCACGGGAT | GTCTGGAAAT | 420 |
| CATAATAGTT | GGCTTAAGCG | GACCAATGTA | GAACGCTTGC | TTCGAGGAAC | TAATCTCATC | 480 |
| GTTGTTATGC | CCAATACCAG | CAATGGTTGG | TACACCGACA | CCCAGTATGG | TTTGTACTAC | 540 |
| TACACGGCTC | TAGCAGAGGA | ATTGCCACAG | GTTCTTGAAA | CGCTTCTTCC | CTAATATGAC | 600 |
| TAGCAAGCGT | GAAAAGACCT | TTATCGCTGG | TCTTTCTATG | GGAGGCTACG | GCTGCTTCAA | 660 |
| ACTGGCTCTT | ACGACAAATC | GTTTTTCTCA | TGCAG | | | 695 |

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1096 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

| | |
|---|------|
| CTCATCCAAG AATAGCATAA AAGAACTCTT CTGTTTTTTC TTGAGGAACG AGAAAGTCAG | 60 |
| CAATCTCCAT TCCACGATCC ATCAAATCCT CTAAAGACAT CGTGATTTTT AAAGTAGTAT | 120 |
| CACTAATTTG TTTCATTTTC ATTGCTAGTA ACCTCATACT TTCAGTTCTA TCTATTATAC | 180 |
| TAGATTTTTA CGATTTTATC AAAAGAAGGC TCCTCTATAC GGATAGATTT TCCCTAGGGT | 240 |
| CTTTCTATAG GAGACTCCAA GAGAAAATTT CTGCAGACAG ATAGAAAAAG CCTCAAAAAT | 300 |
| CGGCTCTTAG CCGATTTTGA AGACCTTATA CATCAGAATA CTTATAATTT AAAGGTTGCT | 360 |
| ACACCAGGA TAGAACGATT TAAGTTTCTG AGAATTTGAA GACTTTGCTC AAATTTCTTA | 420 |
| TAACGAATTC ACTCCGACT CTTCAACAAG AAGGACTGTA TCTCTTTCCA AAAGAGATGA | 480 |
| TACATCTGC AAATCTACAA ATGCATTCCT TTTAAAGCTT CTTGACTCTG TTTCAATTTA | 540 |
| TCTAGGATAG CTTTATTTGA GCTAACGATG GTCAATTCCT GTCCAGTATT TTTGTATGAC | 600 |
| AAAACATCTG CTAGGTTAGC AATTGTTGTA ATCTCTGTTA CAAAATCAAT TTGATACTGA | 660 |
| GAAAAATCAC CTACTCTATT GATTGTTGGA TTAAAGAGAT AACTAACAC ATTTCCCATC | 720 |
| ACAACCAAAA TCACACAAAC CACTCCAATA ACAACTAAAC GAAGAATCAG ATTTTTCACA | 780 |
| TTTAAGCCAA GCGCTGTTTC ACCATTTGCG TTCAATTCTT TAGAGTTGAT GGTTCAGT | 840 |
| TTTTCAATTT TCACATTGTC ATAAGCATGT TTAAATTTCT CAATCAACCC ATCAATTTT | 900 |
| TTCTCTAACA AGTCATTGGC ATCTTTACTT GATGTCAAAA TTTTCACACC AACCCTGCA | 960 |
| TCGTCAATCA TATAGTAGAC GGTCAATTTT TTCCACCAAT AGTCATTTCG TGAATTTTTC | 1020 |
| AAGGTTGTTT CCGTCGTGTC TAATTCACG GCAATTTTTC TCAACTCACT GGGTTCTACA | 1080 |
| TCATTGAAAA GATAAG | 1096 |

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1037 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

| | |
|---|-----|
| TCCCCATCCC AGTGGGCAGC AGCATTAGTC TGTACTTCTG CGTCGTTGCG TTTTATTAGA | 60 |
| AGACTGATTT TGCTTTGAAC TACTTGAAGC TGTCGTTGTA TCCTGCGAAG TTTTGTCTAA | 120 |
| CTTCAGTTTC ATTTGCAGCG ACATGACTAG TTGCCAAGCC TAGTAAACAG ATACTTGCTA | 180 |
| ATCCAATTTT TGTTTTCAAT CTTTCTCTC CTATAAAAA TGTAACAGAC ATCTGAATGC | 240 |

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|------|
| TGTTCCACCT | AGCTTTTGCT | ACTTACTGAT | TATTTTACAA | AGTCAAGCAA | AGCCAAGAAG | 300 |
| CTTTCAGCTT | CAAGTGACGC | ACCACCTACA | AGGGCACCCT | CAACGTCTGG | GCAAGCCATG | 360 |
| TATGAAGCAA | CATTTTCAGG | TTTAACAGAA | CCACCGTATT | GAACACGAAC | TTTGTCTGCG | 420 |
| ACTTCTTGAC | CAAAGTCAGC | AGCTACAACG | TCACGAACAA | CTTTACACAT | TTTTTGTGCA | 480 |
| TCGTCTTGTC | AAGCTGATTT | ACCAGTACCG | ATAGCCCAGA | TTGGCTCATA | AGCGATAACT | 540 |
| GAGGCAGCAA | CTTGTTTCAGC | AGTCAATCCA | GCCAATGCAG | CAGATACTTG | AGCACCTACG | 600 |
| AATTCAGCAG | CTTTACCAGC | TCGTAAAGTT | TCAAGTGATT | CACCACAACA | GATGATTGGA | 660 |
| AGCATACCGT | TCGCAAAGAT | TGCTTTTGCT | TTTTTGTGTA | TATCTTCGTC | AGTTTCATGG | 720 |
| AAGTAGTCAC | GGCGTTTCTG | AGTGACCGAT | AACAACGTAG | TCAGTACCGA | TTTCTTTCAA | 780 |
| AACTTGTTGG | CTAGTTTCAC | CAGTGAAAGC | ACCTGCATTT | TCTCCGTAGC | AGTTTGTGAGC | 840 |
| AGCGACTTTT | AAGTTTGAGC | CTTNGGCAAC | AGCAAGNACA | GTTGTCAAAT | CAAGAGCTGG | 900 |
| AGCAGNGATA | CCTGCTTCAA | CAAGATCTGA | TGAAGGAAGT | TTTGATGCAA | CTGCTTCAAC | 960 |
| GAATGNTCCA | GCTTNTTGGG | GATTTTGTG | CATTTTCCAG | TTACCAGCGA | TAAATGGTTT | 1020 |
| ACGTGACATT | TCACATA | | | | | 1037 |

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| CTTATCGTAC | TAAGGATGGC | AGTGTTCAAC | TGTTCCGTCC | TGATGAAAAT | GCTAAACGCC | 60 |
| TGCAACGTAC | ATGTGACCGT | CTCTTGATGC | CAACAAGTTC | CGAACAGACA | TGTTTGTAGA | 120 |
| AGCTTGTAAG | GCAGTTGTCC | GTGCGAATGA | AGAATACGTA | CCACCATACG | GAATAGGTGG | 180 |
| AACTTTATAT | CTTCGCCCTC | TTTTGATGCG | TGTCGGAGAT | ATTATCGGGG | TAAAACCGGC | 240 |
| AGAAGAGTAC | ATTTTCACCA | TCTTTGCTAT | GCCAGTTGGA | AATTACTTTA | AAGGTGGTTT | 300 |
| GGTCCCAACC | AACTTCTTGA | TTCAGGATGA | GTACGACCGT | GCAGCACCAA | ATGGTACAGG | 360 |
| TGCGGCTAAG | GTTGGTGGAA | ACTATGCTGC | AAGTCTCTTA | CCAGGAAAAA | TGGCCAAGTC | 420 |
| ACGCCATTTT | TCAGATGTTA | TCTATCTGGA | CCCATCAACT | CATACAAAGA | TTGAAGAAGT | 480 |
| CGGATCAGCT | AATTTCTTTG | GAATTACAGC | TGATAATGAA | TTTGTAACAC | CATTGAGTCC | 540 |
| ATCTATCTTG | CCATCTATTA | CCAAGTATTC | CTTGCTTTAT | TTGGCAGAAC | ATCGCTTGGG | 600 |
| ATTAACCTCT | ATTGAGGGTG | ATGTTCCAAT | TGATAATCTT | GACCGTTTGT | TAAAGGCAGG | 660 |
| TGCCTGTGGT | ACAGCAGCGG | TTATTTCTCC | AATTGGAGGT | ATTCAACATG | GTGATGATTT | 720 |
| CCATGTTATT | CTATAGTGAA | ACAGAAGTAG | GTCTGTGAC | ACGTAAATTA | TATAATGAAT | 780 |
| TGACGGGTAT | TCAGTTTGGC | GATATTGAAG | CCCCAGAAGG | TTGGATTGTA | AAAGTAGATT | 840 |
| AAAATAAACC | AAAGGAGATT | TTTTATGAAA | TAGAAAAAGT | GCTTCTTAAC | AGCAGGAGTG | 900 |
| GTCTTGAGCA | CGTCAGCTAT | TTTAGTGGCT | TGTGGAAAAA | CTGATAAAGA | AGCAGATGCA | 960 |
| CCGACAACAT | TTTCTTATCT | CTATGCACTA | GATCCAGCAT | CATTGGGCTA | CAGTATAGCG | 1020 |

| | |
|---|------|
| ACTCGAACAT CGAGGACAGA CGTTATTGGA AATGTTATTG ATGGTTTGAT GGAAAATGAT | 1080 |
| AAATACGGCA ATGTTGCTCC TTCTCAAAAA GACTATGATT TGAACAGTAC AGGATGGGCT | 1140 |
| CCAAGCTATC AAGATCCAGC GTCTTACTTG AATATTATGG ATCCAAAATC TGGTTCTGCC | 1200 |
| ATGAAACACC TTGGCATTAC GAAAGGAAAA GATAAGGATG TTTGTAATA AACCTGGTTT | 1260 |
| GGATAAATAT AAGAAATTGT TAGAAGATGC TGTTCCTGAG ACCACTGACC TAGAGAAGAG | 1320 |
| ATATGAAAAA TATGCCAAAG | 1340 |

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| | |
|---|-----|
| CTCTGACGGC GTCGCCACTT AAGAAGAGTA TCAAAAAGAA AAATAGAAAA TTAATAACA | 60 |
| AGGNAGAAAA ACACATGTCT AAAATTATCG GTATTGACTT AGGTACAACA AACTCAGCAG | 120 |
| TTGCAGTTCT TGAAGGAAGT GAAAGCAAAA TCATCGCAAA CCCAGAAGGA AACCGCACAA | 180 |
| CTCCATCTGT AGTCTCATT CAAAAACGGAG AAATTATCGT TGGTGATGCT GCAAAACGTC | 240 |
| AAGCAGTCAC AAACCCAGAT ACAGTTATCT CTATCAAATC TAAGATGGGA ACTTCTGAAA | 300 |
| AAGTTTCTGC AAATGGAAAA GAATACACTC CACAAGAAAT CTCAGCTATG ATCCTTCAAT | 360 |
| ACTTGAAAGG CTACGCTGAA GACTACCTTG GTGAGAAAGT AACCAAAGCT GTTATCACAG | 420 |
| TTCCGGCTTA CTTCAACGAC GCTCAACGTC AAGCAACAAA AGACGCTGGT AAAATTGCTG | 480 |
| GTCTTGAAGT ANGACGTATT GTTAACGAAC CAACTGCAGC AGCTCTTGCT TATGGTTTGG | 540 |
| ACAAGACTGA CAAAGAAGAA AAAATCTTGG TATTTGACCT TGGTGGTGGT ACATTCGACG | 600 |
| TCTCTATCCT TGAATTGGGT GACGGTGTCT TCGACGTATT GTCAACTGCA GGGGACAACA | 660 |
| AACTTGGTGG TGACGACTTT GACCAAAAAA TCATTGACCA CTTGGTAGCA GAATTCAAGA | 720 |
| AAGAAAACGG TATTCGACTT GTCTACTGAC AAGATGGCAA TGCAACCTTT GAAAGATGCG | 780 |
| GCTGAAAAAG CCAAGAAAGA CCTTCTGGT GTAACCTCAA CACAAATCAG | 830 |

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

| | | | | | | |
|------------|------------|-------------|-------------|-------------|------------|-----|
| GTGGTGGTTT | GACTGCCCTT | ATCGAAGCAG | GTTTCGAANT | CTAAGACANA | AGCAGGTTAC | 60 |
| GCTCCAGAAT | TGGCTTAACT | TTGAAGTTCT | TCACGGAAAT | GAAATTGATC | GTTGACTTGA | 120 |
| TCTACGAAGG | TGGATTCAAG | AAAATGCGTC | AATCTATTTT | AAACACTGCT | GAATACGGTG | 180 |
| ACTATGTATC | AGGTCCACGT | GTAATCACTG | AACAAGTTAA | AGAAAAATATG | AAGGCTGTCT | 240 |
| TGGCAGACAT | CCAAAATGGT | AAATTTGCAA | ATGACTTTGT | AAATGACTAT | AAAGCTGGAC | 300 |
| GTCCAAAATT | GACTGCTTAC | CGTGAACAAG | CAGCTAACCT | TGAAATTGAA | AAAGTTGGTG | 360 |
| CAGAATTGCG | TAAAGCAATG | CCATTTCGTTG | GTAAAAACGA | CGATGATGCA | TTCAAAATCT | 420 |
| ATAACTAATT | AGAAATATAT | AGCGCTGGAG | ATGATTTTAT | GAAAAAGATT | ATGAGAAAAA | 480 |
| TTGCATCGTT | ATTATTGGTT | CTAGTTGTAT | AATGTAATTA | CACCGTCGGT | AATAGTGCTA | 540 |
| GCAGACCAAA | ATAAAGCAGA | TTGGTCGTAT | GATGAAAAATA | CTGTAATTAA | CATTTATGAT | 600 |
| GATGCTAATT | TTGAAGATGG | TAGGTTGCAT | ATGACCTTTG | AACAATTCTT | CAAATTGGCA | 660 |
| CAAATAG | | | | | | 667 |

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|------|
| CGGTTCCAGA | NACTGGTATG | GCTAGGAGTC | GCGACAAAGT | GTATCTTATG | ATGGTCGATT | 60 |
| TGATACTCAA | TACGCTCAAT | ACTTACGGAA | AGAATAAACG | ATCATTGTCA | ACCGGAATAG | 120 |
| TATGATAATC | GTTTCTTGGT | GGAATAAGTT | CAATCTTATC | CTTCTTAGGC | ACAATAATGG | 180 |
| AAGAGCCCAG | TGTTTCGATAA | ACACGATTAT | TAAGGCTGGC | AATTTCCGTT | AATTGCAAAG | 240 |
| CTTCAATGGT | AGGGTGTAAG | ACAGCACCAC | CAAGAGACTA | GTTATAGGCA | GTACTACCAG | 300 |
| TCGGTGTCGA | AACTGTTAGC | CCGTCTCCAC | GAAAACGTTT | AAAGGGAACA | CCATTTATTA | 360 |
| CAATATCTGC | CACCATGGTT | CGATCAGACC | TGCGGATGCT | GGCTTCGTTG | AGTGCTCTGA | 420 |
| AAATCTTAAC | TTCACCATTT | TCAAGAAAGA | CCTTCACATT | CAGAACAGGG | TAAGAAACCC | 480 |
| TTGCCCCAGT | ATCTAGCTGC | AAATTAGTCA | CTAGCTTGTC | CAACTCAAAA | TCACGATAAT | 540 |
| CTGTATAGAA | GCCCAAATGT | CCAGTATGAA | GACCGATAAA | GCGGACCTTG | TCAAGCTGAT | 600 |
| TTTCGTAATT | ATGAAAGGCC | GACAAGAGCA | TACCATCCCC | GCCAATGGAA | ATGACAATAT | 660 |
| CCGGATTGGT | ATCATTGAGT | TATAAACTGA | TTTCTCTTCA | AACGATCTCG | CAATTCATAC | 720 |
| AAAACCCTTT | GACTCTGCGG | TTTTCTATTG | GCTATCAGAT | CAATTCGTTT | ACCTGTATTC | 780 |
| TTCATCTGTA | TCGTCACGTG | NTCCAACACC | GTCATTTAAT | TTTCTACTCA | AAGGATCAAA | 840 |
| AAGTGCCTGG | GCTTCTTGGA | TATCATCACG | AATTTACACC | ATTTCTTCAT | CCAAGTATG | 900 |
| GGCGATTCTA | GCTGTAATTT | CCAGTCGCTT | CTTAATCTCA | TCTGGGAAAT | CCCCTTGGTA | 960 |
| CTGTAGTTG | AGAGAAATGTT | CTATCGTTGC | CCAGAAATTC | ATGGCCAAAG | TACGAATTTG | 1020 |

| | |
|---|------|
| AATTTCTGCC AAAATAGTCT TAGCTCCATT GATGGTATCA ACCGTATATT CTA | 1080 |
| CTACTACCAC ATGATAGGAA CGATAGCCTG ATGCTTTTCT ATGAGTAATG TAATCTCGCT | 1140 |
| CCTGTATGAT TCGCATATCC TGACGCTTGT GCAAAATATC CACTACTTCC TTGACGTCAT | 1200 |
| CTACAACTG AACCATCACA CGTAAGCCAG CAATATCCTG CAAATCGTGT TCCAAGGTCG | 1260 |
| CATAAGTAAT GCCACGACGA GCCATTTTTT CTTTGATGCT CTCAATTGGC TTGACTCGAC | 1320 |
| CGGTCACAAA CTCAATTGGA GAATGCTTAT TTTGCTTACG ATATTGCTTA CGAATACCAC | 1380 |
| GAAGTTTAAT CTTTAACTCA CCAACAG | 1397 |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

| | |
|---|-----|
| CTCCCATGAC ACCTGCACGC TCCGTACGGG CCACGTGCTT TTTAATCCGT TCAACA | 60 |
| ACTT CATAACCCGC TTCAACATCC ACACCCGACT GGGCATATGC ATTTTATTTT | 120 |
| GTCATTGTGTT TTTTCTTTT CTTAATGGA GAATCTGTCG CCTACTTGTA AAAACTGGTC | 180 |
| TTTTCTTCCA AACTTCTACG ATAGTCTTCT TCGTAGTCAT AGAGAGGCGT TGGGTAGTCA | 240 |
| CCGTCAAAGT AAGCGACACA GAGACCACCG TTCGGCGCAT CTGTTTCGAT ACCAATCGAC | 300 |
| TCAATCAAGC TATCAATTGA AAGATAAGTC AGACTGTCCG CACCAATGAT TTGGCGAGTT | 360 |
| TCTTCGACCG TATGATTGGC TGCAATCAGC TCCTGACGGG TCTGGATATC AATCCCGTAG | 420 |
| AAACATGGAT ACGCTAGTGC AGGACTTCCA ATGGCAACGT GAACCTCAGT CGCACCCGCT | 480 |
| TCTTTCAGA GCTGAACGAT ACGACGAGAG GTTGTTCCAC GTACAATGGA ATCATCCACC | 540 |
| ATGACCACAC GTTTGCCTTT GACAACACCC GAAACAGCAG ACAGTTTCAT CCGCACTCCT | 600 |
| TGCTCCCGCA ATTCTTGAGT CGGTTGGATA AAAGTTCGCT GGGTGTATTG GTTTTGTATC | 660 |
| AGACCCATTT CATTTGGTAA GCCTGATTCT TCCGCAAATC CCATAGCCGC GCTTAGGGAA | 720 |
| GAATTGGGCA CACCAACTAC AATATCTGCC TCATGCTTAA ATTCTCGCGC CAATTGCGCT | 780 |
| CCCATTCTCT TACGTGCCGT ATGGACATTG ACCCGTGCAT ATTAGAATCA GGGC | 824 |

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

CTTCTTCCTT GGTACTTCCT CAATTGGATT ACCTTTGGCA TTGCTAGTTT TTCACTCCTA    60
CCTTATATCC AAGGCACTAA AATTATGTTT TACCGAGCAG TATTGGCTCG AAAACGTCCA    120
AAAGCTTGAA GGTTTTCCCC TCAAGCTTTT TTCTATCAAT GAATTTCTCC GCCTACCAAC    180
GTGAGTTCCT GATCTCCATG TTCTATCATA GCGCCGATTG CTGCTTCTAT CCCTCGCCGA    240
ATATCCACTA AACTCATAGT TGGAGTAGTC GGTCTGTTCA CCACCTGTTC CATCATATAA    300
GGAATATGCA TAAAACCTGC CTTAACATAT GGAATTTTCT TTTCTACCAA ATAGAGAGCC    360
TGATACATCA AATGACTGCA AACAAAAGTC CCTGCACGTA TTGGAAACAG ACTGCCGGTA    420
AGTCCTTCTT TTTTATTAGC TTGTACCATC GCTTTGATAG GTAAACTACT AAAATAGGCC    480
GATGCTCCAT CAATACGAAT CGGTGTATCA ATTGGTTGAT TGCCTTCGTT ATCAGGTATG    540
CGAGCATCAT CTTGATTAAT AGCCACTCGT TCAGGTGTTA AGCCGGTCCT GCCGCCGTCT    600
TGTCCAATAC AAAGTACAGC ATCTGGTTGA TATCGTAATA TTTCTGCCTC TAAAACCTCT    660
GACGACTTAT AAAAAACCGT TGGAATTTCT ACCCAGCGAA CTCAGCCCC ATTAATCTCA    720
GATGGTAATA ATTTTACAGC CTCCAAAGCT GGATTAATCT TTTACCTCC AAAAGGATTA    780
AAACCTGTAA CCAATATTTT CATTTTATTT TCCTTTACTA AAATGCGAGA AAGTACATTA    840
AGAATATGTG AATAACAATC ATTACTAGAG CAACACCTGC TTGAGCCTTT ATAACGCCAT    900
TCTGATCTTT CATATCCATC AATGCTGCTG GTAGAGCGTT AAAATTAGCA GCCATTGGGG    960
TCAATAAGGT CCCACAATAA CCTGCTGTCA TGGCAAGAGC ACCAGCCACA ATTGGATTAG   1020

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(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

CTCGTAAAAA CACTAAAGGA GGTAAATAAC CAATGTTAGT ACCTAAACGT GTTAAACACC    60
GTCGTGAATT CCGTGAAAAA ATGCGCGGTG AAGCAAAAGG TGGAAAAGAA GTAGCATTCTG    120
GTGAATACGG TCTTCAAGCT ACAACTAGCC ACTGGATCAC TAACCGCCAA ATCGAAGCTG    180
CTCGTATCGC CATGACTCGT TACATGAAAC GTGGTGGTAA AGTTTGGATT AAAATCTTCC    240
CACACAAATC ATACACTGCT AAAGCTATCG GTGTGCGTAT GGGATCTGGT AAAGGGGCAC    300
CTGAAGGTTG GGTAGCACCA GTTAAACGTG GTAAAGTGAT GTTCGAAATC GCTGGTGTAT    360
CTGAAGAGAT TGCACGTGAA GCGCTTCGAC TTGCTAGCCA CAAATTGCCA GTTTAAATGT    420
AAATTCGTAA AACGTGAAGC AGAATAAGGA GAAGGCATGA AACTTAATGA AGTAAAAGAA    480
TTTGTTAAAG AACTTCGTGG TCTTTCTCAA GAAGAACTCG CGAAGCGCGA AAACGAATTG    540
AAAAAAGAAT TGTTTGAACT TCGTTTCCAA CCTGCTACTG GTCCAATTGG AAACAAACAG    600

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(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

CTTCAGCGAC ATATCTATCC ACAACTTCTC TCGATTCATG TTCCTCTGAA AATGCCTGAA      60
ATTTTAATG  ACTAATTTGA TCCTGATACG AACTATCTGC TAACAAAAC TCAAGATGGG      120
AAACATTTGC TAACGATAA  GGTCTTCTAT CCTTACCTAA CCAAGTTTCT GTCTCTTCAT      180
CCTCTATTAG TCCCCAGTTA CTGGCAAAGT CAGGATGATT CTCTAAAAA ATACGTTCTG      240
TCTGAAAAGT GACTGACCGA ATGGGAAAG  AAGCTGTTCC TCTCTCAAAA CTAGTAAACA      300
ATGCACGCGC AATCCCCTGA  CGGCGATGAC CTGGATGAAC CAGTATCGTC ACTTCTACAT      360
CTTGGTCATC TGCATAGACA GTTAATAAAC CAACAAGTTC GCCTTTTTC TAATAAAGGA      420
AAAAGGCGGG CATGTTTGA  TCAAAATTAA GCATGTTAGA GAGATAGGGA TCGCGATAGG      480
TACCGTCATA GTTTTGGCAA CAGTTAATTA CTTTTTTCGC CTCAGATAGC TCTTCTTGGC      540
TTAACTTGTT TCTTGCTTGA ATCATATAGG TATCCTCTAC AAACCAGACG ATCTGTGACT      600
GGCATCTTTA GCCTGCTCGA GTTTATTGAC ATAATACTCC CGTTTTTCTT CGACTTCGTG      660
AATAACAGGC TCATCTTTCT TACCATGAAG ACGGACAATC TTGGCCGGAA TACCGACAAC      720
CGTCACATCA CTAGGTACAT CTGCTACGAC AACTGCTGCA GCACCGACCT TGGCATTTC      780
ACCAATTTCC ACAGGCCCGA TAAGTTGGGC ATGGGCTGAT ATGAGGGCTC CCTTTCGTAC      840
AGTCGGATGG CGTTTGCCAC AGTCTTTCCC TGTCCCCCG AGAGTCACTC CGTGATAGAG      900
AAGAACGCCT TTTTCAACAA TCGCTGTCTC TCCAATCACC AGACCAGAAC CATGGTCAAT      960
AAAGACACCT GAATCAATCT GGGCTCCTGG ATGAATCTCA ATCTGAGTCC AAAAGCGCCA      1020
AAACTGACTG TGCATACGAG CTAAGAGTTT GAAGTCGTAC TTCCAGAGAA AATGCGAGAG      1080
ACGGTGGGCC GCCAAGGCCT TGACACCTGG ATAAGTCAGC AAAACCTCCA AAGTGGTGCG      1140
GGCCGCTGGA TCATTTTCTT TTACGATATC AATGGTTTCG CGCCACCACC CCATACATTT      1200
CTCCTTTTCT TACTCTGAAT CTT                                     1223

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(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGTGAGTGCC | TTTATTAGCG | GAGCTTCTCA | AGTGATTGTT | GCCTTGATTA | TCTTCCTTTC | 60 |
| ATGCTCTTTT | ATCTCTTGCG | TGATGGGAAA | GGCTTGCGTA | ACTATTTGAC | CCAATTCATT | 120 |
| CCAAGCAAAT | TGAAGGAACC | TGTTGGACAA | GTTCTATCAG | ATGTGAATCA | ACAGTTGTCC | 180 |
| AACTATGTTC | GAGGGCAAGT | GACAGTGGCT | ATTATTGTAG | CAGTAATGTT | TATCATCTTC | 240 |
| TTCAAGATTA | TTGGTCTACG | CTATGCGGTT | ACGCTGGGGG | TTACTGCTGG | TATTTTAAAT | 300 |
| CTGGTCCCTT | ATCTTGGTAG | CTTTCTAGCC | ATGCTTCCTG | CCCTAGTATT | GGGTTTGATT | 360 |
| GCTGGTCCAG | TCATGCTTTT | GAAAGTAGTG | ATTGTCTTTA | TTGTAGAACA | AACTATTGAA | 420 |
| GGCCGTTTTG | TCTCTCCATT | GATTTTGGGA | AGTCAATTAA | ACATCCACCC | TATTAATGTT | 480 |
| CTCTTTGTTT | TGTTAACTTC | AGGATCTATG | TTTGGTATCT | GGGGAGTTTT | ACTTGGTATT | 540 |
| CCGGTTTATG | CCTCTGCTAA | GGTGTGCATT | TCAGCCATTT | TCGAATGGTA | TAAGGTAGTC | 600 |
| AGTGGTCTAT | ATGAATTAGA | GGTGAGGAA | GTCAAGAGTG | AACAATAGTC | AACAGATGTT | 660 |
| ACAGGCTTTG | GAGGAGCAAG | ATTTAACTAA | GGCTGAGCAT | TATTTCCGCA | AAGCTTTAGA | 720 |
| AAATGATTCA | AGTGATCTTC | TGTATGAGTT | GGCAACTTAT | CTTGAAGGGA | TTGGTTTCTA | 780 |
| TCCTCAGGCC | AAGGAAATTT | ACCTGAAAAT | TGTAGAAGAT | TTCCAGAGG | TTCATCTTAA | 840 |
| TCTAG | | | | | | 845 |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

| | | | | | | |
|------------|------------|------------|-------------|-------------|------------|-----|
| CTATGGATTA | ATCTTCTTCT | ATCTTATCCT | GTTCCCTAAAT | ATGTTGGTAG | AAAAATGAAG | 60 |
| CAGTTGTTAC | GAGTGTCTGT | ATTGGAAAAA | AATTTTGTCT | ATACAATTCT | TTAAATGATA | 120 |
| TGAAGACTAG | GAATGCCAAA | ACACTGACAT | ATTTCTGTTA | AAGCCTATCC | AGTCTCTTCA | 180 |
| ATTGTATTTG | TAGAAATGCT | ATCAGTAATA | TATTCGCGAA | CACATATGATT | TACAACAGTG | 240 |
| TGGTCGTACA | TCTTTGTAAC | TTTATTATAC | AACAACCATT | TACAGGTGTA | AAGTTGAGCA | 300 |
| GTGTCTTTAG | TAAATTTAGG | GACTTGTTTT | GTCATAGTTT | TGATACCTGT | ATTCGTTGTT | 360 |
| TCATGAGTAT | TTGACGTTTC | TTTTCATGTA | GGCATTTCAA | CAATTAGAAT | GATATTTTTC | 420 |
| CGAGGATGAA | CTTATATATT | ATGACTTTTT | AGAGTTATGA | TGCCTCTTGA | TTTGACTATC | 480 |
| GCTATCAATT | TCATCCACTT | TTACAGTTTC | ATGCAACATA | GCGAGAAGGC | GGTTTCCTAT | 540 |
| ATGGAAGTCG | TCTTGTTTTC | ATATTGTCTA | AATACGAGAT | ATTTACTACA | GGTTGTAGAT | 600 |
| ATTGCAAGCT | CAAATGATAT | TATTTTAGAG | GAGGAGACAA | GTGAAATAAT | GCCTGGTGAG | 660 |
| TTAGATGAAA | TAAAAAGTAA | GGAGTTGAAA | GTACTGGTTC | NTTGTGCAGG | GTCTGGAACA | 720 |
| AGTGCGCAAT | TAGCCAATGC | AATTAACGAG | GGCGCTCNAT | TAGCAGAAGT | TAGAGTGATT | 780 |
| GCGAATTCAG | GACCGCACGG | AG | | | | 802 |

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

CTGGGACTCT CTTCTAGAA GTCATGCAAG AATATTTTGA TCAAAAGAGG AAATCATGAA      60
AAAAAGAGCA ATAGTGGCAG TCATTGTACT GCTTTTAATT GGGCTGGATC AGTTGGTCAA      120
ATCCTATATC GTCCAGCAGA TTCCACTGGG TGAAGTGC GC TCCTGGATTC CCAATTTCGT      180
TAGCTTGACC TACCTGCAAA ATCGAGGTGC AGCCTTTTCT ATCTTACAAG ATCAGCAGCT      240
GTTATTCGCT GTCATTACTC TGGTTGTCGT GATAGGTGCC ATTTGGTATT TACATAAACA      300
CATGGAGGAC TCATTCTGGA TGGTCTTGGG TTTGACTCTA ATAATCGCGG GTGGTCTTGG      360
AAACTTTTAT GACAGGGTCA GTCAGGGCTT TGTTGTGGAT ATGTTCCATC TTGACTTTAT      420
CAACTTTGCA ATTTTCAATG TGGCAGATAA CTATCTGACG GTTGGAGTGA TTATTTTATT      480
GATTGCAATG CTAAAAGAGG AAATAAATGG AAATTAAAAT TGAAACTGGT GGTCTGCGTT      540
TGGATAAGGC TTTGTCAGAT TTGTCAGAAT TATCACGTAG TCTCGCGAAT GAACAAATTA      600
AATCAGGCCA GGTCTTGGTC AATGGTCAAG TCAAGAAAGC TAAATACACA GTCCAAGAGG      660
GTGATGTCGT CACTTACCAT GTGCCANAAC CAGAGGTATT AGAGTATGTG GCTGAGGATC      720
TTCCGCTAGA AATAGTCTAC CAAGATGAAG ATGTGGCTGT CCTTAACAAA CCTCAGGGAA      780
TGGTTGTGCA CCCGAGTGCT GGTCATACCA GTGGAACCCT AAGTAAATGC CCCCCATGTA      840
TCATATTAAG GACTTGTCGG GTATCAATGG GGTCTGCCT CCANGGATTG TTCACCCGTA      900
TTGATAAGGA TACGTCACGT CTTCTCAT                                     928

```

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

CTCTTTTACA GAGGTGTTTC CTATTTTGTG CTTCCATTTT TGGGGCAAGG AATTGTAGAT      60
GGGGATGGCA ATCCTATCTT TTTATTGATT ATGATATTCG TTTGCTTCAT AGTTTTAGTC      120

```

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| TTTTTGAAAT | GGTTAGACTA | TGATTTCACT | AGATTGAGAA | GGGAGTTTCT | AGATACAGGT | 180 |
| TTTCAAAAGT | CTCTTACTAA | GATTAAGTGG | GCAATGGGGG | CTTATTATCT | AGTGATGCAA | 240 |
| AGTCTATCTT | ACCTTGAATA | TGAACAAGGT | ATTCAATCAA | CGACTGTTCTG | CCATCTCATC | 300 |
| CTAGTGTTTT | ACCTACTCTT | TTTTATGGGG | GGTATCAAGA | AATTGGATAC | CTATTTGAAG | 360 |
| GAAAAACTTC | AGGAGGAACT | GAACCAAGAG | CAGACCTTGC | GCTACAGAGA | TATGGAACGC | 420 |
| TATAGTCGGC | ATATAGAGGA | ACTTTACAAG | GAAATTCGGA | GTTTTCGCCA | TGACTACACT | 480 |
| AACCTCTTAA | CCACTTACGT | TTGGGCATTG | AAGAGAAGGA | TATGGAGCAG | ATAAAAGAGA | 540 |
| TGTACGACTC | GGTCTTAAGG | GATTCCAGTC | AGAAATTGCA | GGACAATAAA | TATGACCTGG | 600 |
| GCAGATTGGT | GAATATTNGT | GACCGTGCCC | TCAAGAGTCT | CCTAGCTGGA | AAATTATATA | 660 |
| AAG | | | | | | 663 |

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| CTAGATTAAT | CTGATATTTT | TTTTTGCCAA | ACCAAATGCT | TCCTATCAGA | AAAGCTAGCA | 60 |
| ACAGCAACAT | GGTAATAATG | ATATGAATGG | TCATTTTCTT | CTCCTATTCT | GCCTTTTCAA | 120 |
| TATCTTTTTT | CATCTCGTCA | ACATTGAACT | TAGCAAACAA | GTATTGACGG | TCTTGGACTG | 180 |
| GGAAACGTTG | GTCCAACCTG | TCAACTGCTC | CCACCTCGAT | AATGCCTTCC | TTGATGACAA | 240 |
| AATCCATGAC | ATGTCCACCG | AAGGTCAAAT | CATCTGATAT | GAAGTGCAGA | TGGTAGCCTG | 300 |
| CCCACTGAC | CCCATGGAAA | ATCTCAGGCG | TCCAGAAACC | AACAATAGTC | CCCGCAACAT | 360 |
| TGTCACGACT | ATATCCCGT | TGATGGGTTG | CGACATCAGC | AACTTGGTA | TCGGGTGTTG | 420 |
| ACTTAGGAAT | CATACGCACA | TGCATATGTT | AAAAATTCCC | CCCCGAATCT | TGATAGAGCG | 480 |
| GAAAAGATTT | TCCCCATCAT | AATAAGACTC | AATTCGTTCT | TTCAATTCCCT | TGTCTGTCAT | 540 |
| CTCAAAGCGC | TGGCGAAAAA | TGACCTCTGC | CTGATGCGGT | ACCACTGCAG | CGTAAGGAAT | 600 |
| AAGGGCATCT | GGTGACACTT | CCACAATTTC | TGGCTGGTCT | CCTGACCCCT | TGG | 653 |

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTACGATATC | TTTGGTCTTT | TGTAAGATAT | GAGGTCCACC | CTTATGCGCC | TCAGTTGGCA | 60 |
| TTTCATGCGA | TTCAAGAAGT | TGCCCCTCTT | GATCAACCAA | ACCATACTTG | ATGTTGGTTC | 120 |
| CACCGATATC | AATTGCAACG | TAATATGTCA | TAAATACCTC | CTTTTAGATT | AGAGGAAGCG | 180 |
| CTCCTTGGTT | TCACGAATCA | AGGCAGCAGC | CGCTTCTACA | ACTGGACGAT | CTTCTTCAGT | 240 |
| CACTGGTGTC | AATGGTGAAC | GAACAGATCC | AATATTCAAG | CCTTCATTGA | TTTTCAAGAC | 300 |
| TTCTTTGATG | ACACCGTACA | TATTTCCATG | AGCAGAAGTG | AGTTTACCAA | TGATTGCGTT | 360 |
| GATAGCATAC | TGCAATTCAC | GCGCTGTTTC | TAGGTCCTTA | TCCGCAATCA | ACTGATTGAG | 420 |
| TTTCAAGAAG | AGTTCTGGCA | TAGCACCATA | AGTACCACCG | ATACCAGCCC | TAGCCCCCAT | 480 |
| GAGGCGTCCT | CCTAGGAACT | GCTCATCAGG | ACCATTAAAG | ACGATATGGT | CTTCTCCACC | 540 |
| AAGGCTGACA | AAGGTTTGA | TATCTTGAAC | TGGCATAGAA | GAGTTCCTCA | CACCGATAAC | 600 |
| ACGAGGATTT | TTCAACATTT | CTGTGTAAAG | GCTTGGAGTC | AAAGCAACCC | CTGCCAATTG | 660 |
| AGGAATGTTG | TAAATCACGT | AGTCTGTGTT | TGGAGCTGCA | GAAGTGATAT | CGTCCAGTA | 720 |
| TTTGGCAACT | GAGTTATTCT | GGCAAGCGGA | AATAAATTGG | TGGAATCCGT | TGCAATAGCA | 780 |
| TCTACTCCCA | AGCTTTCAGC | ATGGCGAGCA | AGTTCCATAC | TATCTTTAGT | ATTATTGCAA | 840 |
| GCAACATGGG | CAATAATGGT | CAATTTACCT | TTGGCTACCG | CCATGACTTC | TTCCAAAATC | 900 |
| AACTTGCGAT | CTTCAACGCT | TTGGTAGATA | CATTCAACAG | AAGAACCATT | GACATAAGAC | 960 |
| CTTGAACACC | TTTATCAATG | AAGTATTGA | | | | 989 |

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TCAAAGAGTA | ACAAAGGCAC | CAAATCTCTG | ATAGGAACGA | TTTAGCACGG | TAAACTTCAT | 60 |
| CCACTTGGGT | TCACGGAACC | AAACCAGCAA | TAATTTCTTT | GGGCACGGGT | TAATAGCATT | 120 |
| TTGGTCAACT | AGGAGTAGAT | AGAACACATT | TCNTTCTTCG | TCTATATCAA | TCTTAACACC | 180 |
| TGTTTCAGCG | ATAATCTTGT | CGATGGTTTC | TCCACCCTTA | CCGATGACAA | TCTTAATCTT | 240 |
| GTCCACATCA | ATCTTGATCG | TATCAATTTT | CGGAGCAGTT | GGAGCCAATT | CTGGACGAAC | 300 |
| TTCTGGAATG | GTTGCTTCAA | TGACATCAAG | GATTTCAAAA | CGCGCTTTCT | TGGCTTGAGC | 360 |
| AAGAGCCTCC | GTCAAGATTT | CTGCAGTAAT | CCCTTGAATC | TTGATATCCA | TTTGAAGGGC | 420 |
| TGTAATCCCA | TCACGAGTAC | CTGCAACCTT | GAAGTCCATA | TCTCCAAAGT | GATCTTCCAA | 480 |
| ACCTTGATA | TCTGTCAATA | CTGTGTAGTT | ATTTCCATCT | GAGATAAGTC | CCATAGCAAT | 540 |
| ACCAGCTACT | GGCGCCTTGA | TTGGCACACC | ACCAGCCATA | AGGGCAAGAG | TTCCCGCACA | 600 |
| GATAGAAGCT | TGAGATGAAG | AACCGTTTGA | TTCCAAAAC | TCTGCTACTA | GACGGATAGC | 660 |

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|------|
| GTATGGGAAT | TCTTCCAAGC | TTGGCAAGAC | TTGAGCAAGA | GCACGCTCAC | CAAGGGCACC | 720 |
| GTGACCGATT | TCACGACGAC | CTGGCGCACC | GTAACGACCT | GTTTCCCCTA | CAGAATATTG | 780 |
| AGGGAAGTTA | TAGTGGTGCA | TAAAGCGTTT | CTTGTA CTCT | GGATCCAAAC | CATCAATGAT | 840 |
| TTGAGTTTCT | CCCATCGGAG | CCAAGGTCAA | GACTGAAAGA | GCTTGAGTTT | GCCCACGAGT | 900 |
| AAAGAGACCT | GAACCATGTT | ACACGAGGAA | GGAAGTCAAC | AACCGCATCC | AAAGGACGGA | 960 |
| TTTCATCGAC | CTTACGACCA | TCAGGACGCA | CCTTGTCCTC | TGTAATTAAA | CGTCGCACTT | 1020 |
| CTGCGTGTTT | CATTTGTTC | AAGATTTCAG | CCACATCACG | CATAATACGG | TCAAATTCTT | 1080 |
| CGTGGTCCGC | ATATTTTCT | TCGTAAACGG | CAGTCACTTG | GTCTTTCACT | GCTTGAGTTG | 1140 |
| CAGTTCACGG | GAATCCAATT | TCTCTTCTAC | TTGAACTGCC | TTTTGGAGGT | CAC'TGTTGTA | 1200 |
| GGCTGCAATG | ATTTCAGCTT | GCAATTCAGC | ATCCACGTGA | AGCAATTCCA | CTTCTGCTTT | 1260 |
| TTCTTTACCG | ACAGCAGCAA | CGATTTCCTC | TTGGAAGGCA | ATCAATTCTT | TGACAGCTTC | 1320 |
| GTGCCCTTTA | AGAAGCGCTT | CCAACATGAT | TTCTTCTGAC | AATTC'TTGG | CACCAGACTC | 1380 |
| TACCATGTTG | ATAGCGTGCT | TGGTTCAGC | TACTGTCAAT | TCAAGAAGAG | ATTGCTCTGC | 1440 |
| TTGTTCTTGA | CTGGGTTGA | TGATGATTTG | GCCATCTACA | TATCCCACTT | GTACCCACAGC | 1500 |
| AATTGGTCCG | TCAAATGGAA | TATCTGAAAT | AGACAGTGCC | AAAGATGAAC | CAAACATAGC | 1560 |
| AGCCATTGGT | GCAGATGCAT | TTTCATCATA | AGAAAGCACT | GTATTGATGA | CTTGGACTTC | 1620 |
| ATTACGGAAA | CCTTCCGCAA | ACATAGGACG | AATCGGACGG | TCAATCAAAC | G | 1671 |

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

| | | | | | | |
|------------|-------------|------------|-------------|------------|-------------|-----|
| CTCAGTATCT | TTGTAATCAA | CATATCCAAT | TTTGT'TTGCT | GCGATGTANT | CAACTTTTTT | 60 |
| ACGGCGTTTG | AATCCGCCAC | GACGTNGTTG | AGCCATGTTT | TTNCTCCTTT | ATAAGTTTAG | 120 |
| TTGTCCATTA | GAATGGTAAA | TCATCANCTG | AAATATCCAA | TGGGTTTGTT | GCTCCAAATG | 180 |
| GATTTTCATT | ACGTGAAAAG | TCTGGTACTG | AATTTGTAGG | TGCTGAATAG | TTTGACGTTG | 240 |
| GTGCAGAGTA | AGCTCCACCT | GTGTGACCCT | CACGCACACT | ACGGCTTTTC | AACATTTGGA | 300 |
| AATTCTCAGC | CACGACCTCT | GTCACGTAGA | CACGTGTGCC | TTGCTGGTTA | TCGTAAC'TAC | 360 |
| GAGTCTGGAT | ACGACCTGTC | ACCCCGATAA | GTGAGCCTTT | TTAGCCCAG | TTAGCAAGAT | 420 |
| TTTCAGCCTG | TTGGCGCCAC | ATAACGACAT | TAATAAAATC | AGCCTCACGT | TCACCATTTT | 480 |
| GACTCTTAAA | TGTACGGTTT | ACTGCAAGAG | TAAAAGTCGC | AACTGCTACA | TTTGATGGGG | 540 |
| TATAACGCAA | CTCAGCGTCA | CGTGTCTATC | GCCCTACAAG | TACAACATTG | TTAATCATAG | 600 |
| TTTACCTTCT | TACGCGTCAA | TTTGTACGAT | CATGTGACGA | AGAATGTCAG | CGTTGATTTT | 660 |
| GGAAAGACGG | TCAAAC'TCTT | TAGAGAGCTG | CATCGNTCAT | TTGCTTCAAC | GTTAACGATG | 720 |
| TGGTAAAGTC | C | | | | | 731 |

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

CTGGGTTTTC CCACGTTTTC CTGATGTACG AGCGAGATCC TTACGGTTCA ACATAGTGTT      60
GATAAAGCTG GATTTACCAA CATTGTAACG CCCTGCTAGG GCAATCTCTG GCAGTTCATC      120
CTGCCGATAG TGGGACTTAT TAGCTGCACT GAGCAAGATT TCAGCATTGT GTGTATTAAG      180
TTCCATAGTC ACCTCTAGGC TGTTCCTAGG ATCGGTTTAT CCGTTCCATC GACAGTTTCT      240
TTAGTGATGC GAACCAATTT CACATTTTCC TGAATCGGCA CCTCAAACAT AACATCTAGC      300
ATGGTTTCTT CGATGATGGA GCGAAGTCCA CGCGCCCTCG TCTTCCGTTT GATTGCTTTA      360
TTAGCAATCT CTTGAAGGGC TTCGTCGTCA AATTCCAACCT CAACATCATC ATAAGAAAGC      420
AAGGTTTGGT ATTGTTTCAC CAAGGCATTT CTTGGCTCTT TCAAGATGCG AACCAAGTCC      480
ATCAACGGAC AATTGCTCAA GAGCCGCAAA AACAGGCAAG CGTCCAATCA ACTCAGGGAT      540
AATACCAAAT TTTTGAATGT CTTCAGCGAT GAATTCCTTG ATGTATGAGC TGTTTCTCTG      600
TCAATCGCCT TATTGTTTTG ACCAAATCCG ATGACTTTTT CACCCAGACG TTGTTTGACA      660
ATTTCTTCAA TACCATCAAA AGCACCACCC ACGATGAAGA GGATATTTTT TGTATCCACT      720
TGAATCATCT ACTTGTTGTG GATGTTTGCG TCCACCTTGA GGCGGCACGC TAGCAACAGT      780
TCCCTCAATA ATCTTGAGAA GGGCTTGTTG CACCCCTTCA CCAGAAACAT CACGTGTGAT      840
AGACACATTC TCACTCTTCT TGGCAATCTT GTCAATTTC A TCCACATAGA TAATGCCACG      900
CTCTGCACGT TCGATGTTAA AGTCAGCAAC CTGCAAGAGT TTGAGGAGTA TATTTTCCAC      960
ATCCTCACCC ACATAACCAG CCTCCGTCAG AG

```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

ATTTTCACAG GGCAGGATGC GGAACGACTA GCCCCATACT TTAACGGAAT TTTGGTAGGG      60
ACAGCTCTTA TGCAGGCAGA AAATGTGCCC CAGAGAATCA AGGAGTTGCA GATTGACAAA      120

```

| | | | | | | |
|------------|------------|-------------|------------|-------------|-------------|------|
| GGTTAAATTT | TGTGGACTAT | CGACCAAAGA | AGCGGTGGAA | ACAGCCGTTT | CAGCAGGAGC | 180 |
| CGACTATATC | GGTTTTGTCT | TTGCACCTAG | TAAAAGACAG | GTGACTTTAG | AAGAGGCAGC | 240 |
| TGAGTTGGCA | AAGCTTATTC | CTGCAGATGT | GAAGAAAGTT | GGAGTATTTG | TTTCACCAAG | 300 |
| TCGGGTAGAA | CTGCTGGAAG | CGATTGACAA | AGTTGGCTTG | GACTTGTTTC | AAGTTCACGG | 360 |
| TCAGGTGGCA | GATGATTTAT | TTGAGAATTT | GCCTTGCGCC | AGTATTCAGG | CTGTGCAGGT | 420 |
| AGATGGAAAT | GGGCATGTCC | CCAATTCTCA | GGCAGATTAT | CTACTCTTTG | ATGCCCCCTGT | 480 |
| GGCAGGAAGT | GGCCAGTCCT | TTGATTGGGG | TCAACTGGAT | ACGACTGGAC | TAGCACAGCC | 540 |
| CTTCTTTATC | GCAGGTGGCC | TTAATGAAGA | TAATGTAGTA | AAAGCAATTC | AACATTTTAC | 600 |
| TCCCTATGCA | GTAGATGTAT | CGAGCGGAGT | GGAGACAGAT | GGACAAAAAG | ATCATGAAAA | 660 |
| GATTAGAAGA | TTTATAGAGA | GGGTAAAGCA | TGGCATATCA | GGAACCAAT | AAAGATGGAT | 720 |
| TTTACGGAAA | ATTCGGCGGA | CGTTTTGTCC | CAGAAACATT | GATGACAGCA | GTTTTGGAGT | 780 |
| TGGAGAAGGC | CTACCGTGAA | AGTCAGGCAG | ACCCAAGTTT | CCAAGAGGAA | TTAAACCAAC | 840 |
| TCTTGCGCCA | GTACGTAGGA | CGTGAACTC | CTCTTTACTA | CGCAAAAAAC | TTGACCCAGC | 900 |
| ATATCGGCGG | AGCCAAGATT | TATCTCAAAC | GGGAAGACCT | TAACCATACA | GGAGCCCACA | 960 |
| AGATTAAACA | TGCCTTAGGA | CAAGTTTGGC | TTGCCAAACG | CATGGGTAAA | AAGAAAATTA | 1020 |
| TCGCAGAAAC | GGGTGCTGGT | CAGCACGGTG | TGGCAACTGC | AACTGCTGCG | GCCCTCTTTA | 1080 |
| ACATGGAATG | TACCATCTAC | ATGGGTGAGG | AAGATGTCAA | ACGCCAAGCC | CTCAATGTGT | 1140 |
| TCCGTATGGA | GCTTTTGGGA | GCTAAGGTTG | AAGCAGTGAC | AGATGGTTTCG | CGCCTGCTCA | 1200 |
| AGGATGCGGT | CAATGCAGCC | CTTCGTTTCAT | GGGTGGCTAA | TATCGACGAT | ACCCACTATA | 1260 |
| TCCTTGGTTC | TGCCTTGGGG | CCTCATCCAT | TTCCAGAAA | | | 1299 |

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1078 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGTTGAATC | AACAACACGT | ATCCAAGTAT | CAGNATCAAA | TTATGCAGGT | AATCGTACAA | 60 |
| TTGGAAATCA | CCGTGGATGG | TTCAATCCAA | CAACAACCTC | TGAAGGTTTT | GTTACATATA | 120 |
| TTTATGCAGA | TTAATTTACA | GAGGGACTCG | AATAGAGCCC | TCTTTTCAGG | TTTTACCGTG | 180 |
| ACAATCCCTA | TTAAAAATTA | TATCAAAATA | GCTTGAAAAT | ATTGGAAAAG | TATGGTAGAA | 240 |
| TGAAAATTGT | CGTGTGAACG | ATAATACTCA | TTCTTGATGA | ATTGTGAAGC | AGTTGCCCTT | 300 |
| GGGTGCTTTT | GCGAGTTGAA | GTCAAGAAGA | GGAAAAAAC | AAAAAGGAGA | AATACTCATG | 360 |
| GCAGTAATTT | CAATGAAACA | ACTTCTTGAG | GCTGGTGTAC | ACTTTGGTCA | CCAAACTCGT | 420 |
| CGCTGGAATC | CTAAGATGGC | TAAGTACATC | TTTACTGAAC | GTAACGGAAT | CCACGTTATC | 480 |
| GACTTGCAAC | AAACTGTAAA | ATACGCTGAC | CAAGCATACN | ACTTCATGCG | TGATGCAGCA | 540 |
| GCTAACGATG | CAGTTGTATT | GTTGCTTGGT | ACTAAGAAAA | CAAGCAGCTG | ATGCAGTTGC | 600 |
| TGAAGAAGCA | GTACGTTTCA | GTCAATACTT | CATCAACCAC | CGTTGGTTGG | GTGGAACCTC | 660 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| TACAAACTGG | GGAACAATCC | AAAAACGTAT | CGCTCGTTTG | AAAGAAATTA | AACGTGGATG | 720 |
| GAAGAAGATG | GAACCTTCGA | AGTTCTTCCT | AAGAAAGAAG | TGCACTTCT | TAACAAACAA | 780 |
| CGTGCCGCTC | TTGAAAAATT | CTTGGGCGGT | ATCCGAAGAT | ATGCCTCGTA | CCCCAGATGT | 840 |
| GATGTACGTA | GTTGACCCAC | ATAAAGAGCA | AATCGCATGT | TAAAGAAGCT | AAAAAATTGG | 900 |
| GAATCCCAGT | TGTAGCGATG | GTTGACACCA | ATACTGATCC | AGATGATATC | GATGTAATCA | 960 |
| TCCCAGCTAA | CGATGACGCT | ATCCGTGCTG | TTAAATTGAT | CACAGCTAAA | TTGGCTGACG | 1020 |
| CTATTATCGA | AGGACGTCAA | GGTGAGGATG | CAGTAGCCGT | TTGAAGCAGA | ATTTGCAG | 1078 |

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTATGAGGGA | TATAAAGTGA | GAGAGTTGGG | CCAACGTTCC | AAAAACGTCC | TAAATTCTGC | 60 |
| CCATTGACAA | AGGCAACCCC | CTTACCAAAC | TCAGACNAGT | CTAGGTAAGT | ATCTTTTGGC | 120 |
| TATTCGACTG | TAAAGTCATA | AGCGTAAAAG | GCTGGTTGTC | CTTGAGTCCA | TCCTTTGGAA | 180 |
| AAATCAATTT | TCTCAGGATT | GTCTAGTGGG | AGTGGATAGT | GTTTCCAGTT | TAGTAAGAAA | 240 |
| TGCAGATCCT | TACAGACCCC | TGTCCGAATT | CCCTTACGTT | GCGTATCCGC | TAAGAACTTA | 300 |
| TGCCCATAGT | TGACACGCCC | CATATTTTCT | ATCAAGATAT | CTAACCTAGA | TAGCCCTTTC | 360 |
| TTTTTACCTT | GATAAAAAAT | ATCTTCCCCA | ATCTCTGTCT | GATATTGAGT | TTTAACCCAC | 420 |
| TGACCATCGA | CATACAGCTG | GGCCCTATCT | CGACCATCAA | TGATACGAAG | TCTTTCTTCT | 480 |
| TCTGCATCCC | AGTTTGTTTC | TGTTGATAA | AGTAGGTAGC | CATAACTTTG | TCCCAGCTCC | 540 |
| TCCATCTTTT | GAGGATAGAG | ACTTTCTACA | GGGACTTGAC | AAGCTATCTA | AGGTTTCAAA | 600 |
| CAAAGAAACT | TTTTCAACTA | GTGGAATAGC | ATCCAACCTC | ATACTCTCTT | TGTAGAGTGG | 660 |
| TTCCAACGTC | GGATACTCTG | AAAAATGTGT | TGCCATCATC | TTCTTGACTG | CAAGATATTT | 720 |
| AGCAGTTGGA | TTTCCTTCTT | CATCCAGAAG | GGCATCGTAA | TCATAAGACG | TTAACTTGTC | 780 |
| GCAGGTCCAA | ATTCCTCGAG | | | | | 800 |

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTCACGCAGT | TCTGTTACCA | AAGACCGTTC | AAAAAGCAAA | CTAGCAATAC | TTATAACTTA | 60 |
| TTAGAAATTC | CTAATTTTAC | CTTGCTAAAC | GAATACAGGT | CACGATGCCA | TCTGAGTCTG | 120 |
| TGATTTCCAA | TTGGCTCGAT | GTCATCCATT | TGATTGGTAC | GTCAACTTCT | TGTGCTCGTT | 180 |
| GGGCAATCGT | TAACAGTTCT | TCTTTATGTG | CAACTTCGAT | GACATAGTAG | GCTAAACCTG | 240 |
| GTAAGCCTTG | CTTACGCGGA | AGCCAGACCT | TTTCCTTCCC | CATTCGTAA | CTGCTAAATG | 300 |
| ATGATGGTAA | TCTCCAGCCG | CAATCCAAC | AGCGCCAGGC | ACACTGAATT | TATTCTCTAG | 360 |
| CCCTAACACC | TTTGATAAA | ACTGGCTGGA | CTTTCGACTA | TCCTTGACGG | AAAGATGAAT | 420 |
| ATGCCCCATT | CTTGACCTT | CTGCCAGGAT | AAAGGGCTCT | ACTCTTCCC | CCAACTCATA | 480 |
| AATGTCCTGC | GCCGCAAGAG | CCTCCGTCAC | TCCGATAATG | CGTCCATCTT | CTCGAATATC | 540 |
| CCATGTGGAA | ACTGGCTTAT | CTCGATAGAG | TTCAATGCCA | TTTCCCTCCA | AATCTTCCAA | 600 |
| GTAAATAGCT | TCACTGTAAC | CATGGTCTGC | ACCGCCGACA | AGAGGAATTT | GCAAATCTGT | 660 |
| CAGATGTTTC | AAGACATCAG | CCAAAGCCTT | GCGTGTGGGC | AAGAGAATGG | CCAAATGGTA | 720 |
| AAGACCATAA | TGTTCCCTCA | CTTCTCCGCT | CTTCTTGTGC | TTGAATCAG | | 769 |

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

| | | | | | | |
|------------|------------|------------|------------|--------------|------------|-----|
| TTACCCCAAG | CCTGCAACTT | CCCAAGCTGA | TGGTTGAAT | GATTGTGCAT | CAACACCACC | 60 |
| AGTATCAGTG | ACGATGCTG | CTTTTGTCTT | CACATCAGAA | GATGAAGCTG | CGTTACGAGA | 120 |
| AGAGCGGTTA | CCACATGCAG | CAAGTCCAAC | TGCTGCCACT | GCAACTAGGC | CAAGACCTAG | 180 |
| CCATTGTTTC | TTGTTCATTA | CTGAACCTCC | TAAATAAGAT | GTGCAACGAT | GTTGCAAGTA | 240 |
| TGGATTGATT | GGTCACAAAG | ACCCTTGCCA | CTCAAAGAGC | GA CT CAGACT | AATTTAAGTC | 300 |
| TGTAAAAGAA | TATGGAAGTA | ACTCCCCGAC | CGTCATCTCG | ACCGTCGATT | TATCTTTTGC | 360 |
| GACTAAGGTC | ACTTTTAAAT | CTTGTTCAAA | AAATTCGACC | ATTACTTGGC | GACAAGCACC | 420 |
| ACATGGTGAA | ATCGGTTTTT | CAGTTTGACC | ATAGACAATC | AATCTGAAA | ATTCTCTTTG | 480 |
| GCCTTCAGAT | ATAGCCTTAA | AAATAGCTGT | TCTCTACCG | CAATTGGTCC | AAAGGATAGC | 540 |
| TAGCATTTTC | GATATTCACT | CCCGTGTTAA | ACATTTCCGT | CTTTGGCTAC | TAAACTGCT | 600 |
| CCGATAGGAA | AGTGAGAATA | GGGGACATAG | GCATGTT | | | 637 |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 940 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| CTGAGGATAA | TGACATCTGC | CANAGGAGCA | AAACTAGCAA | AATCATCNGT | TGCACGGTCA | 60 |
| ATCATGCCTT | CTTTCAAGGC | GATATCTCTC | GAAGCTTGAC | TACGGATTAT | AACCTAAAT | 120 |
| TTCATAATCT | GGATGATCGC | GTTTGATACC | AAGTGCCATA | GAGGCTCCAA | TCAACCCAAG | 180 |
| ACCTGCGATA | TAGATTGTTT | TTGCCATAGG | AACTCCTTAA | TAGTTCTTTG | TATAGTCTCG | 240 |
| GTGTTTGGCT | ACCGCTTCTT | TTAGTTCCTC | AAGATTATCT | GATGAGAATT | TTTCGAGGAT | 300 |
| TTCTTGCGCC | AGAACCGTTG | CTACAACCTG | TTCCATGACC | ATTCCTGCAG | CTGGAAGAGC | 360 |
| AGTCGGATCA | CTTCTCTCCA | CGGTTGCCTT | GTAAGGTTTC | TGGGTTTCGA | TATCCACACT | 420 |
| CATAAGAGGT | TTATAAGAG | TAGGAATGGG | TTTCATGACC | CCACGAACAA | CGATGGGTTG | 480 |
| CCCATTAGTC | ATACCACCTT | CAAAACCACC | TAGATTATTG | GTACGGCGAG | TATAACCGTC | 540 |
| TTCTTTAGAC | CAGAGAATTT | CATCCATAAC | TTGGCTGCCT | TTACGATAAC | CAGCCTCAAA | 600 |
| GCCAAGACCA | AATTCCACCC | CTTTAAAGGC | ATTGATAGAG | ACAACAGCTT | GAGCCAATCT | 660 |
| TGCATCCAAT | TTTCTATCCC | ATTGGGACAT | AGGAACCAAG | ACCAACTGGG | AACGCCTCCG | 720 |
| ACGACTGTCT | CCACAACCCC | ACCGATGGTA | TCACCATCAC | GTTTGATTTG | GTCAATATAG | 780 |
| TCCTTGATTT | CCTGTTCTCG | TTCTTGGTTG | ACAATAGAAA | ACTTCCAGAC | TGGGCAGCTC | 840 |
| TTTGCTTTAA | TTTCCAGCGA | CTGTCAGATT | TTCCAGGAAC | ATCCATTCCC | TTGCCACCAA | 900 |
| AGACCACGAC | ATGGTTGGCA | ATCTCCATAT | CCAGATTCTGA | | | 940 |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GATTCTACAG | GATCCATTTT | ACTATCTTAC | GCGCCGGGAA | GTAGGCTGAG | ACATAACCAA | 60 |
| GTAATAGAGC | CAACAACCTAG | AGTTCCTAAA | ACAGATAAAA | GATTTAATTC | AAAAACCTTA | 120 |
| GTGATGGATG | GGTAAAAGTG | ACTTACAATC | GCATTCGCCA | AACTTCCCAC | CCCTTGTGCA | 180 |
| ACCAAAAATG | CCAGCAGCAA | GCGATGCGCT | ACAATCCAGA | TAGCCTCGTA | AATAAAAATT | 240 |
| CCTTTGACAT | CACGATTCTG | ATAACCAACT | GCTTTCATGA | CACCTATTTT | CTTGAACGT | 300 |
| TGCATGATAT | TGATGTAAAT | AATGATACCA | ATCATAACCG | CTGCTACCAC | AATAGCTTGT | 360 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GATGAAAGCA | CAATCAATAA | TCCCTGAATA | ACACGAATAA | AGGTAATCAC | AATATCAAGA | 420 |
| ACTCTCTGTT | AAGAAAGCAC | AGTATACTTC | TTATTTTCT | GTAATCTTC | TGTTACTACT | 480 |
| TTTGTCTGTG | ATGGATCTTT | GAGTTCCAAG | ATAAATAAG | ATACAGCTTT | CGTAAATCCA | 540 |
| GCCTCTTTCA | AAATCGTTTC | CATTTGATGA | GACAGCATGA | AACTGTTGCT | GTCTCCATG | 600 |
| TCATCTTCAT | CATTGATTAC | ACGTACAATC | TTCGTTTGAA | ATTGAGCAAT | CTTACTAGTT | 660 |
| TCGGCAGCAC | TTTCTACAAT | GCTGACTGAG | ACTGATTTGC | CAATAAGATC | ATTAGCTGTC | 720 |
| AAATTTTTTC | CTGTCTGTTT | ATTCCAATTT | TTTAGTAAAG | CTGCTTGGA | TCGTTAATCC | 780 |
| CTGTTTCAAT | GTATCAGTAT | AGAGGGATCC | AGCCAACACT | TTGTCCGTCT | CATTATTACT | 840 |
| AACAGAGATA | CTTGTATCAT | CATAAAGACT | CACTACTTGA | GCATAAGAAG | CATCGTTTGA | 900 |
| CTCAATCCA | TTTCTTGCCC | ATCTTTTCTT | GCCCATCTAT | AGTAATATTT | GACATGTTCA | 960 |
| TCCCNAAAGG | ACTCTCCAAA | TATNNNATAG | | | | 990 |

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

| | | | | | | |
|-------------|-------------|------------|-------------|------------|------------|------|
| ATCGGCTAAG | ATGCGTGGAG | CATCACAAAT | TATCCTTATG | AGCCGTCATG | AAGACGTCAA | 60 |
| AAGATGGCTA | TGGAGTCAGG | TGCGACAGCT | GTGTGTCAG | AACGTGGTCA | AGAACGAATT | 120 |
| ACCAAGGTGC | GTGAAATCCT | CGGCGGAGGA | GCAGACGCAG | CACTTGAATG | TGTTGGTACG | 180 |
| GAGGCTGCTA | TAGAACAGGC | GCTAGGTGTT | CTTCATAATG | GAGGGCGTAT | GGGCTTTGTA | 240 |
| GGAGTCCCAC | ACTATAATAA | TCGTGCTCTT | GGTTCGACAT | TTATGCAAAA | TATCTCTGTA | 300 |
| GCAGGTGGGG | CAGCTTCTGC | TACAACATAC | GATAAGCAAT | TTTTACTAAA | AGCCGTCCTT | 360 |
| GATGGTGATA | TCAATCCAGG | TCGCGTCTTT | ACTTCAAGTT | ATAAACTGGA | AGATATCGAC | 420 |
| CAAGCCTACA | AAGATATGGA | TGAACGTAAG | ACCATTAAAGT | CTATGATTGT | AATCGAATAA | 480 |
| AAAACGAATA | GGAGTTTATG | AACTCTATTC | GTTTTTTATG | TTATCCTATT | CTTGATTTAA | 540 |
| GGTACTTTCT | CTTAATGTCA | GTCTGGTTCC | CAGCATGGTC | AGGCTAGGGA | TTTTCCGACC | 600 |
| GTGGAGGACT | TCCTTGTTAA | GAATATCCAT | ACCTGCTCGG | CCCATTCTCT | CAGTATAAAC | 660 |
| TGTAATACTA | AGAGAGGGGA | GGATAGACCT | GTTTGGTTCAG | ACTAAGTGTC | GTAAAAAGGA | 720 |
| AAATGAGGCT | GACGCGATCT | GGCAGGCTGA | TTCCAGCTTC | TTGGAGGGCA | CGGAGGGCAC | 780 |
| CGATAGCTAA | ACTATCGCTG | GCTGCGAAAA | ATGCTGGCGG | AAGTTGGTCT | CCCAAGCTCT | 840 |
| GAATGGCCTC | CTTCATTAAAG | TCATAGCCAG | ACTGGGCAGT | AAATCTTCCT | TGAAAGACCA | 900 |
| GTTTCATCATG | ATAGATTCCC | CTCGCTTGAC | TGTAGTTTTT | GAAGTTTTCT | AGACGCTTGT | 960 |
| CCTGAATGAT | TTCTTCTTGG | TCTGTAGTTT | CTTCAAGGCC | TGTTAGAATC | CCGATACGGT | 1020 |
| CCATTCCCTG | ACTGAGGAAA | TAATCGACAA | CCTGTTTCAT | AGCAGTGTA | AAATCCGTGA | 1080 |
| TAATACAGGT | ATGTCCCAGG | GAAAGTGTAT | CGCTGTCTAG | AAATACAAGA | GGCTTTTGST | 1140 |
| ATTCTTCAAA | GGCAGAAATC | TGAGCTTCTT | GATAGGATTG | ATTCTGCTAG | GGATAACAGC | 1200 |

CAAAGGCAAT CCTCCCTTTA TCCACCTCAT ATTTGAAACC ATTCAGCTC TTA

1253

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```

CGTGTACCAT CAAGAGGCTA ATTGATGTTT CTTCCCCCTG TGCCTCTCTT GTCAACATTT      60
CTGTTTGAGC CTTATGCGCC TGTATAAGG CAGCATTTCG ATCAGCTAAT CTTGATTGG      120
CTTTAGAGAA ATCCCCTTT TTTGCTGCCT GAATAGCCTC CATAGCATTA CTTTGGCTT      180
CCCCACCATA CATAATTAGC CCCATTACAG ATTCTAAATT ACTTTCATCC ATAACATTCT      240
CCTCAATCTT AGTCTAATAA ACTTTCAGCT AAATCTAAGA CTTTAGAACC ATTCATCATT      300
CCATAATCTG TCATCGGAAT AACCGCCACA GGAATCTGTC TATCTTTTAG TTTTCTTGA      360
AAGTCCCCTA GTAAATAGCG AACTTGAGGA CCTAAAAGCA ACACATTTAC TTCTTTTGTT      420
GCTACAATTT CTTCTGCTTC AGGAGCTGGA ACTGCAAAA TTTCTGCATC CAACCCCTTA      480
TCTTCTGCTG CCTTTTGCAT CTTTGTCACT AGCAGACTTG TACTCATACC TGCTGCACAT      540
GCTAACATAA TTGTTACTTT AGCCATAGCT TACTCCTTTA TCACCTATTT ACTGACCTAG      600
CCAAGCGAGA TACTGTATGT CTCCTCCTC TAATGTCCTT GCTCAATGCA TAAATATTAT      660
CGACTGTTGC CAGTCCCCCA TATCCTGCGT CACCTATATG TTGAATATCA ACTCCACAAA      720
TTTATTCTT AAGTGCAATT TCCTTAATAG TATCTGTATC AGATGTTTCT TGGCTAGTAC      780
CAATAGCACT CAATACAAGA CCACCCTTAC TATGAACGAG ATCAACGACT TCACGCAACT      840
CTTGGTCATG AAAGGCTGGA ACGGTTCCAA CTGCTGGAAC AAGTATCACA TCCGCACCTG      900
CTTCCAACAA TTGCTCTGCG ACAGAAAGCT CTGCCACAGG CTCATTCACT CCTGCCCCGT      960
GCATCTTACC TGCAATAATC AAACCAGAAA AGTTTTCCTT AGCAGTTTGA ACAGCCTTAA      1020
TGATTTCTCG ATTGCTAACT CCTGTTCCAG GATTTCAGT CAAACAGACA AAGTCAAAAC      1080
CTAACTCCTA TATTCGCTTC AATGTTTCAA CACTAGCAAC ACGACCTGCA ACAATTTCTT      1140
GTGTTTCCTC TAGCATTCTT TGCAGATGGG TCAATCGGTT CCAAATTTAC ACCAATTGGA      1200
CAAGCAACAA G                                     1211

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(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

CCACACTAGC AGCCTATGGA CTCACTAAAA GAAAAGAAGA CTAAGTCTTT TCGATAAAAA    60
ATAAACAGCG AGATTGAAGC TCGCTGTTTA TTTTAAATT AATCACCTAG TCCAAGACGT    120
TCAAAGATAT CATCCACTCG TTTGGTGTA TAAACTGGGT TGAAGATTTT ATCGATTTCT    180
TCTTGTGTGA GACGTGATGT TACTTCTGAA TCTGCCTCAA GAAGTGGTTT AAAGTCTACT    240
TGTTGTCCC AAGAGTAGGC TGTTTTGGT TGCACCAAGT CATAGGCTTG CTCACGGGTC    300
ATGCCTTTT CAATCAATGT CAACATAGCC CGTTGGCTAA AGATAAGACC AAAAGTCGAG    360
TTCATGTTT GGATCATATT TTCTGGGAAG ACTGTCAAGT TCTTGACGAT ATTTCCAAAA    420
CGTTGAGCA TGTAGTCAAT CAAAATGGTC GTATCTGGTG TGATGATACG CTCAGCTGAT    480
GAGTGAGAAA TATCGCGTTC GTGCCAGAGA GCGACGTTT CATAAGCCGT AATCATGTGA    540
CCACGAATGA CACGCGCCAG ACCAGTCATA TTTTCAGAAC CGATTGGGTT GCGTTTGTGA    600
GGCATTGCTG AAGACCCTTT TTGCCCTTTA GCAAAGAACT CTTCTACTTC GCGTTGCTCA    660
GATTTTGTGA GACCACGAAT CTCAGTCGCC ATACGTTTCA TTGAAGTCGC AATGCTGGCA    720
AGAACCGBAA AGTACTCAGC GTGAAGGTCA CGAGGAAGGA CTTGTGTAA AGATTCCTTG    780
GGCACGGATG CCAAGTTTAT CGCAGACATA CTCCTCTACA AATGGTGGGA TATTGGCAAA    840
GTTCCCAACC GCACCAGAAA TCTTACCAGC TTCTACACCA GCAGCCGCAT GCTCGAAGCG    900
CTCCGATATT GCGTTTCATT TCGCTGTACC AAGTTGCTAA TTTAAGGACC AAAGGTTGTC    960
GGCTCAGCGT GCACACCATG AGTTACGCCC CATCATGATG GTGAACCTGT GCTCCTTGCG    1020
TTGTCAGCGA TGATATTAGT GAAGTTTCA AGGTCACGAC GGATGATGTC GTTGGCCTGC    1080
TTGTAGAGGT AACCATAAGC AGTATCCACC ACGTCGGTAG AAGTTAACCC ATAGTGAACC    1140
CACTTGCGCT CTTACCAAG AGTCTCAGAA ACCGCACGCG TGAAAGCCAC CACATCGTGG    1200
CGCGTCTCCT GCTCAATTTT CAAAATACGG TCGATGTCAA AGTCCGCCTT CTTGCGAATC    1260
AAAGCCACAT CTCCTTAGG GATTTCCCA ACTCAGCCCA TGCCTCGTCA GAGAGGATTT    1320
CCACCTCAAG CCAAGCACGG TATTTATTTT CTTCACTCCA AATATTCGCC ATCTCAGGGC    1380
GAGAGTAACG GTTGATCATG TGTTAATTTT TCCTTCTTC TTAAG                1425

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(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

CTATTCTGAG TATAAAGTTG GCGGAGGCTG GAACTACGCT CGTTATGAGG TCATAAACTA    60
CTATACGGGA GGTTATTAAT CCTTAAAGAG TGAGAAAAGG AGGGCTGGAT ATGTTAAATC    120
TTACTCATGT TACCTTAAAA ACGCGACAAG TCATCTTGCA AGATGCGGAT TTTACCTTTA    180

```

| | | | | | | |
|------------|------------|-------------|------------|-------------|------------|------|
| AAAAGGGTAG | GATTTATGGC | CTTCTTGCTA | TCAATGGCTC | GGGAAAGACG | ACACTATTCC | 240 |
| GAGCTATGAG | CAAGTTGCTT | CCCCTTAGTA | GTGGACACAT | CGCAGTTCCT | CCTTCTTTGT | 300 |
| TTTATTATGA | GAGCGTTGAA | TGGCTGGATG | GAAACTTAAG | TGGGATGGAC | TACCTTCGTC | 360 |
| TCATAAAAAA | ACATCTGGAA | GTCAGACCTA | AACTTGAGAG | ATGAAATCGC | CTACTGGGAA | 420 |
| ATGGCTGACT | ATATCAGTCT | TCCCATCCGC | AAGTATTCCT | TAGGGATGAA | GCAACGCTTG | 480 |
| GTGATTGCTA | TGTATTTTCT | CAGTCAGGCC | AAATGCTGGC | TCATGGATGA | GATTACAAAT | 540 |
| GGCTTAGACG | AGTATTATAG | ACAGAAGTTT | TTTGATAGGC | TAGCACAAAT | CGATAGACAA | 600 |
| GAACAGCTGG | TTCTTTTAAG | TTCCCACTAT | AAGGAAGAGT | TGGTTGATAT | CTGCGATAGA | 660 |
| GTAGTAACCA | TTCATCAGGG | GCAGATAGAA | GAGGTTTAGT | TTATGAAAGA | TGTTAGTCTA | 720 |
| TTTTTATTGA | AAAAAGTTTT | CAAAAGTCGT | TTAAACTGGA | TTATCTTACT | TTTATTTGCA | 780 |
| TCTGTACTCG | GTGTTACCTT | TTATTTAAAT | AGTCAGACTG | CAAACCTCAGT | CAGCTTGGAG | 840 |
| AGAGAGTTGG | AAACTCGTCT | TGTAGACCGT | GAGAGAGTCA | TCAATGAAAA | TGAAGAGAAA | 900 |
| CTCTCCCAA | TGTCTGATAC | CAGCTCGGAG | GAATACCAGT | TTGCTAAAAA | TAATTTAGAC | 960 |
| GTGCAAAAAA | ATCTTTTGAC | GCGAAAAGACA | GAAATTCTGA | CTTTATTAAA | AGAAGGGCGC | 1020 |
| TGGAAAGAGG | CCTACTATCT | GCAGTGGCAA | GATGAAGAGA | AGAATTATGA | ATTTGTATCA | 1080 |
| AATGACCCGA | CTGCTAGCTC | TGGCTTAAAA | ATGGGGGTTG | ACCG | | 1124 |

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| CAGAGCAACT | TCGTCAAATC | TTCATAGGTG | AGGTAACCAA | TTGGAAAGAG | GTTGGTGGTA | 60 |
| AGGACTNACC | CATCTCTGTT | ATCAATCGGG | CAGCCGGCTC | TGGCTCTCGT | GCTACCTTTG | 120 |
| ATACTGTGAT | TATGGAAGGT | CAGTCTGCCA | TGCAAAGTCA | GGAGCAGGAT | TCAAATGGAG | 180 |
| CGGTAAAAATC | AATCGTATCA | AACAAGTCCA | GGAGCTATCT | CTTATTTATC | TCTTACCTAT | 240 |
| ATAGATGATT | CGGTCAAAAG | CATGAAGTTG | AATGGCTATG | ACTTAAGTCC | AGAAAATATA | 300 |
| AGTAGCAATA | ATTGACCCTT | GTGGTCTTAT | GAGCATATGT | ATACATTGGG | GCAGCCCAAT | 360 |
| GAGTTGGCTG | CAGAATTTCT | CAATTTTGTT | CTCTCGGATG | AGACCCAAGA | AGGGATTGTC | 420 |
| AAAGGATTGA | AGTATATTCC | GATTAAGGAA | ATGAAGGTTG | AAAAAGATGC | TGCCGGAAC | 480 |
| GTGACAGTGT | TGGAAGGGAG | ACAATAATGA | ATCAAGAAGA | ATTAGCTAAG | AAAATGTTGC | 540 |
| TTCCATCAAA | GAATTCTCGT | CTGGAGAAAT | TAGGAAAAGG | TTTGACCTTT | GCCTGTCTTT | 600 |
| CTTTGATAGT | CATCCTTGTT | GCCATGATTT | TGTTTTCGT | AGCGCAAAAA | GGCTTGTCGA | 660 |
| CCTTCTTTGT | CAATGGTGTG | AATATCTTTG | ACTTTCTTTT | GGGAGGAACT | TGGAATCCTT | 720 |
| CTAGTAAAGA | ATTTGGTGCC | CTTCCTATGA | TTTTGGGTTT | CTTTATCGTT | ACCATTCTCT | 780 |
| CAGCCCTTAT | CGCAACACCC | TTTGCTATTG | GTGCAGCAGT | TTTTATGACC | GAAGTATCAC | 840 |
| CAAAAGGGGC | GAAGATTTTG | CAACCAGCTA | TTGAACTCCT | GGTTGGGATT | CCTTCAGTAG | 900 |

| | |
|---|------|
| TGTACGGATT TATTGGCTTG CAAGTCGTCG TTCCCTTTGT TCGCAGTGTC TTTGGTGGGA | 960 |
| CTGGTTTTGG GATTTTGTCA GGGATTTCG TCCTCTTTGT CATGATTTG CCGACCGTAA | 1020 |
| CCTTTATGAC AACGGATAGC TTGCGTGCGG TTCTCCNTT ATTATCGTGA AGCCAGTTTC | 1080 |
| GCTATGGGA | 1089 |

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

| | |
|--|------|
| CTNTNTTTAA ACCTTGACCT TANTTGANNA TTATACCGAA ATNTCTTCA TTTTAAAG | 60 |
| AAAAAAGGGC GCTGGTAAAA GGGATAATCT TCACCAACTC CCTATNTTC TACTTATCTA | 120 |
| AGCCTAATTC TGCCAAGATT TGACGTTTGT NGGCAATCTT TNGGACTTCN TNGTCCTCAT | 180 |
| CTTCAGACCA GTCTAGTTTA ATTTCTGAAA CAATCTGCCC AGGGNGATTT NTCAAGATAT | 240 |
| AGATGCGGTC GCTGAGANTG AGGGCCTCCT CAATACTATG CGTGANGATC AGGGTTGTTA | 300 |
| GCTGCAACTG CTTGTGAATC TCAAGATACC AAGCGTGGAG TTCCATCTTT GTCATCTCAT | 360 |
| CCAAGGCGCT AAAGGCCTCA TCTAAGAGAA AGAGCTTGTG CCCAAAAGG TAGGTCCGGA | 420 |
| GTAAGGCTAC ACGCTGGCGC ATCCCACCGC TAAGTTCATG AGGATACTTG TCTCTTACAG | 480 |
| CTGTCAGCTG GAAGGTCGCA AGAATTTTAT CCGCTCGGGA AATAGCTTCT GCCTTATCCA | 540 |
| CCTTTTGAAT CAAGAGGGGC AGAATGATAT TTCCAAGCAC CGTCTTGTGC TCCAAGAGCA | 600 |
| GATCCTTTTG CAACATATAA CTCACGTGCC CCTTGGGATT TTCTTCACCA TCAAGGACAA | 660 |
| TTCTCCCTGA CTGAACTTCT AAAATCCCAG CGATTAGATT AAAGAGGGTG GTCTTTCCAA | 720 |
| CACCACTTGG GCCTAGGATG GAAACCACCT CGCCTGAAGT CACCTGTAGG TTGATATCCT | 780 |
| CTAAAATCCT CTCCTGACCA TAGGCATAAC TGACGTGCTC TAGTCTAATT TCTGTCAATTA | 840 |
| TTTCACAAAT TCGTTGGTGA AGCCTTTGTC TGTCAAGTCT TCTTTAAGGA TACCATTTTC | 900 |
| TTTATCCCAT TTATAGAAAG CATTCACCG AGCTGCGTCA AATTGACCCC ATTTTCCCTT | 960 |
| GTCGCTTGCG TATCTTTTGA ACAAGTATTT TTGAGATTG ATGACAAAGT CACGTTTTC | 1020 |
| CTTGAGTTCA GGTGCATTCT TGATGAGAAT ATCTGCAGCT TCTNCTGGAT GTTCCATGGC | 1080 |
| ATATTGGTAG CCTTTTNTGA TGGCTTGGAT GACTTTGCGA GCTTCTTCTT TGTTATCTTT | 1140 |
| CAGATAGTCG TTGTTTGCGA TGATAACTGG TGAATATTAN TCAAACCTCT TGACATAGTC | 1200 |
| TTTCAANTAC ATGAAGTTAG CATCTACACC TTGAGATTTA GCAAGGATAC CATCCCAACC | 1260 |
| GTAGTAAATC CNAGCAGTAT CAAAGACGCC ATTGGCAATC GGTGTGATTG AGTTTGAGTC | 1320 |
| NTTANTTGGT ACTNTTTCAA CCTTCTCACA GTCTCCNCCT TGAGATTCTA CCAAGGTTTT | 1380 |
| CAACATACMN GTTCANTTGG GTCATTCAT GTCCCATATT TCTTACCAAC CAAGTCTTTT | 1440 |
| GGACTGCCTA CATNTTCACA TTACCGAGAG ATGATCCCTG ATGTATTGTG TTCCACCNAT | 1500 |
| AG | 1502 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

ACTCTTCAGC GATTTCTTGG CTGAGAATGT CCTCATAGGC AGGGAGTTGG ATGTCCTGAC      60
CATATTTCTT CTTGAGGGCA GTAGTAACTA GGCATAAGC CAGATTGGCA TTACGAGAGA      120
AGATAGGCCC GNGGAANTAC GAACCAAAGA CATTCTTATA ATGAACCCCT TCACCGACCT      180
TTTCTTCGTT GTTTCCATTT CCATAGACAA CCTGTCCCAG CGGTTTTTGG TCATCAGAGA      240
GGAAGGTACG ACCTTGGTGA TTTTCAAATC CATAGTAGGT TTCATCGAAA TCTTTCATTG      300
TGAATCTTGA TGTCACCGAT AAAACGGTTA TTGGTCTGGT TGAGCGTGTA GTGTCCCATG      360
ACCCCTAGCC CTTGATACG TTTTCTGAA GCTTCAACAT AATATTGACC CAATAGTTGG      420
AAACCACCGC AGATAGCCAG AACTACACCG TCGTTTTGGA TGAGTTGTC AATGCTCTCT      480
TTTTTAGCAG GTAGGTCGTC TGCAATGATA CTTTGTTCAG AGTCTTGACC ACCACCGAAA      540
AAGGCGATGT CGTAGTGATT TTCATCAAAG TCATCATGGA GAGAAACGAT GTCAACGGTC      600
ACATGGGTTC CCAGTTTTTC AGCCACATAC TTGAGCATGA GGATGTTTCC ATTGTCCCCG      660
TAGGTATTCA TGAGATTTCG GTAGAGGTGG GCAATGTTGA GCTGATAGGG GTAATTGCCA      720
TCTTTTGAGG AAAGTGAAGT ATAAACCATT AGTTCATCTC CTTTCTAACA ATCTGACGAC      780
TAGCCAGCAG TTCACGAAAT TCCAGCATGG CAGTATAAGT TGCCAGAATA TAGGCATGCT      840
TGCAGTCTTG ATTCTCAATG GTCTTGAGAA CTTGCTCCAG ATTACTCGTT TCAGTGATTT      900
TCTCAGCTGG ATAGCCAGTC ACTCGGAGGC GACGAGCGAT TTCAGAATGA CGAACACCGC      960
CAGCGTTGAT TTCAGGAATG TCCATGTCAG TGATTGCTC AAAGTCTGCA TCCCAGATCC     1020
AG

```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

CCTCCAGGTC TCGGGAAACG ACCATGGCCT TTGTTATTGC CAACGAACTG GGAGTCAATC      60

```

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|------|
| TTAAGCAGAC | GTCGGGTCCA | GTCATTGAAA | AAGCCGGAGA | TCTGGTAGCT | ATTTTGAATG | 120 |
| AGTTAGATCC | TGGGGATGTA | CTTTTATTG | ATGAGATCCA | TCGTTTGCCA | ATGTCAGTGG | 180 |
| AAGAGGTGCT | TTATAGTGCT | ATGGAGGACT | TCTACATAGA | TATTATGATT | GGGGCTGGTG | 240 |
| AGGGTAGTCG | TAGTGTTCAT | TTGGAGTTAC | CACCTTTTAC | CTTGATTGGT | GCGACGACTC | 300 |
| GGGCTGGTAT | GCTCTCCAAT | CCGCTACGGG | CACGTTTGG | GATTACAGGC | CATATGGAGT | 360 |
| ATTATGCCCCA | TGCTGACTTG | ACAGAAATTG | TCGAGCGGAC | GGCAGATATT | TTGAGATGG | 420 |
| AAATCACTCA | TGAGGCAGCA | TCTGAGTTGG | CCCTACGTAG | TCGTGGGACC | CCTCGTATTG | 480 |
| CCAATCGTCT | CCTCAAGCGC | GTGCGCGATT | TTGCCCAGAT | AATGGGGAAT | GGGGTAATTG | 540 |
| ATGATATTAT | TACCGATAAG | GCTTTGACTA | TGCTGGATGT | TGACCATGAA | GGTTTGGACT | 600 |
| ATGTGGATCA | AAAAATCCTT | CGTACCATGA | TTGAGATGTA | CAGTGGAGGA | CCTGTTGGTC | 660 |
| TAGGAACCTCT | TTCTGTTGAA | TATCGCCGAA | GAACGTGAGA | CAGTTGAAGA | TATGTATGAG | 720 |
| CCTTACTTTG | ATTCAAAAAG | GTTTTATCCA | TGCGGACACC | GTCCTGGACG | GGTGGCGACT | 780 |
| GCCTAAGGCA | TATGAGCACT | TAGGTTATGA | ATACAGTGAA | AAATAAGCAA | GAAATCCTTA | 840 |
| GAGGCTTTTT | AGAGAAAATC | CAGATATGAT | GGCCATTCTG | ACGATCATCC | GAGACCTTGG | 900 |
| TCTGAAAGAC | TCGTGGTTGG | CAGCAGGTTT | TGTCAGAAAT | TTCAATTTGGA | ATCTTTTGTC | 960 |
| AGACAAATCC | CCTTTTGATC | ATGAAACAGA | TATAGATGTT | GATTTTCTTT | GATCCAGAT | 1020 |
| TTTTCTTATG | AGGAAACCTT | ATTACTGGAG | AAAAAGCTGT | GAGAGGATTT | TCCTCAGTAC | 1080 |
| CAGTGGGAAT | TGAAAAATCA | GGTCTATATG | CATCAGCACA | GTCCTCACAC | TGCTTCCTAT | 1140 |
| ACCAGTTCTC | GTGATGCTAT | GAGTAAGTAT | CCAGAACGGT | GTACGACAGT | TGGACTGCGC | 1200 |
| TTGAATGAAG | AATCAGATTT | TGAACTCTAT | GCACCTTATG | GTTTGGAGGA | TATTTTGAAT | 1260 |
| TTCAAGTTCG | TCCAACCTCT | CATTTCTTAG | AAAATGAAGA | CCGAATGGAA | CTCTATCAAA | 1320 |
| CACGTTTATC | CAAGAAAAAT | TGGCAGGAGA | AAT | | | 1353 |

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTCCTGGAAA | TTCTGGCAAG | TAGGCTGGAT | GAATGTTGAC | AATCCGACCT | TCATAAGCCG | 60 |
| ACAATAAGGT | TGGTCCAACG | ATTTTCATGT | AGCCTGCTAG | GCAAACCAAG | TCAATCTGGT | 120 |
| GTTCTTCCAA | GAGTTCGACA | AGGGCTGCTT | CGTAGTCTGT | CTTGCTCTCA | AACTCCTTGA | 180 |
| GTTCAAAAGC | ATAGGACAGA | ACGCCGAGCT | GCTTTGCACG | CTCAAGCACA | TAGGCATCAC | 240 |
| GATGGTCTGA | AAAGACAAAC | TCCACTGGAA | ATTCTTCGGC | AATCACCTGA | AAATTTGAGC | 300 |
| CATTACCAGA | GGCAAAAACC | GCTATTTT | TCATTTGATA | ATGACACTTT | CGTTTCTTTT | 360 |
| CTTGACGATG | CGACCAATTT | CATAGACTGC | TTCATCCAAC | AATCTTTT | CACGCTCTAC | 420 |
| ATTTTCAGGG | CTGACCGCCA | ACATAAGTCC | CACACCCATA | TTGAAGATTT | CAAACATTTT | 480 |
| TTCGTGTTTA | ATCTGACCAT | ATTTTTCALG | GGCTTTGAAA | ATTGGAAGCA | CTGGAACTTT | 540 |

GCTTTCATCA ATTTTCAGCAG

560

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

| | |
|---|-----|
| CTTCAACACT TTATTTTAT CTTTCTCCA TTTCGTATGC TAGTTCGGAA ATTGTTGCTA | 60 |
| GAACCTCTCC GACTATTTGG GATGTTCTCA TTGCTTTTGT AGGAGGGATA GCAGGTATTA | 120 |
| TTGGTGCTAG GAAAAAAGAG ACCAATAATA TTGTTCTTGG TGTGCTATT GCAACCGCCT | 180 |
| TGATGCCTCC TCTTTGTACA GTAGGTTATG CTATTGCTTC TGCTAATCTA AAATTTATCA | 240 |
| TTAGGCTCCT CTTACCTATT CCTCATCAAT TGTAGCTTTA TTGTCATTGC GACTTATATA | 300 |
| GGTGTTAGGT TGATGATGGT TAAGAAACAT TATTTTAAAG ATAATGAAGA AGACTCTAAA | 360 |
| ATGCGTAGGA TTTTGCTTCT AGTTGCTGTT TTGCTGATGA TTCCGAGTTT CATCTCTGCA | 420 |
| ACGACTTTAG TGAGAGAAAC GTTGAAAAAA GAGTCCCTTA AGAAATTTAT ATCAGAGCAG | 480 |
| TTTCAGGGGC ATAATATTTT GAAAAAAACC TATTCTAAAA AGACTCATAC CCTAAAGCTA | 540 |
| ACCATTTCAG GAAATTATTT GACAGAAGAA GAACTCGATA TGATTTCAAG TAAGAGAGGT | 600 |
| GACTATGGTT TAAGTGATGT TTCTGTTCAA GTTTCACAAT TGTCTGATTC AGAACAACCT | 660 |
| AGTAAGGAAG AACTGGTGGA GTATTTCTTC CAGTATATCA AGGATAAGGA AGCAAAAGAA | 720 |
| AAGGAAAAAG CTAATAAGTT TTATACAGAG TCTGAGGAGC AATAATTTCT TGAGAATAGC | 780 |
| TGGTTTTTCT CGTGAGTCTT CTATGTATAT CAAAGGAAGA CTGAGGTTTT AAGTATGAAA | 840 |
| CTTTTCTTCT ATTATAGTAG | 860 |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

| | |
|---|-----|
| TCTTGGCCAA CTGCATGGAG TTCAGCGGTC AATTTCACG CACCTGAGAA ACAGACCCCT | 60 |
| GCACCCCTGA AATCTCAGGA GACATGATGG TCTGGATGGA ATCAATAATG AGAAAGTCTG | 120 |

| | |
|--|-----|
| GCTGGATACG CTACCACTTC TGCACGAACA CTCTGCATAT TGGTCTCTGC ATAGAGATAA | 180 |
| AACTCACTAT CAAAATCACC TAAGCGCTCT GCACGTAGTT TAATCTGCTG GGCAGACTCC | 240 |
| TCCCCACTGA CATAGAGAAC TGTCCTCCACT TGGGACAACT GGGTTGAGAC TTGTAGGAGA | 300 |
| AGAGTTGATT TCCCAATCCC AGGATCCCCA CCGATGAGGA CGAGACTTTC CTGGTACAAC | 360 |
| TCCGCCTCCA AGCACACGGT TGAATTCCTC CATCTCCGTC TTGGTTCGAT TGACATTGAT | 420 |
| GGAAGTCACC TCAGCTAGTT TCATGGGCTT GGTTTTCTCA CCTGTCAAGG ACACACGCGC | 480 |
| ATTCTTGACC TCGGCAACCT CAACCTCTTC CACAAAAGAA GACCAAGACC CACAGTTGGG | 540 |
| GCAACGTCCC AGATATTTAG GGAATTATA CCCACAATT TGACATACAA ATGTCGCTTT | 600 |
| TTTCTTTGCG ATGACAAACC TCTTTCTATA TCTCTAACTC AACTCAATC ACTTGGCAAA | 660 |
| AATCAATCTT CTCATTTGGC ACAAACCTGGC GCATGAGCAT TCGATGAGCA ACAACTACCA | 720 |
| CAGTCTGATG TTCTCGATAC TTAAACATAC ATTCTAGAAA CCGAGACTTC ATTTCCGTAG | 780 |
| CTGTCTCATA TTGAATAGGA CTATTAGGAA GCAACTCCCC CTGTGTTTCT AAAAACAGTC | 840 |
| TTCTAGCTGT TTCAAAGTTT TCTATTCCTG TTTTATAGAC CTGCCATTCA TGTAATAAAG | 900 |
| GCTCTACTCT TAAAGGAAGA CCCGT | 925 |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

| | |
|---|-----|
| TTCTNGATCA AGTCAAGGAC TGCANGCCAC GACCGACATA GCGTTTGGCA ATGGAAACAA | 60 |
| CCAAACGAAG ATTGGCTTCC GCAAGACGTT GTTTGGCTTC GATATCGCCA GCTTCAACAG | 120 |
| CCAGTGCCAA CTCTTTCTCC TCTTCATTGG TCAAGAGAGG AACGACCCCT ATTTCTTTCA | 180 |
| AGTACATACG GACAGGGTCA TTGACCTTAG CAGAAGTTGA CCCAATCAAG TCCTCATCGC | 240 |
| TGAGTTCTGG TTCTTCTTCA TTGCTAAGAA CACGCGCACT TGGATTTCTT TCGTTATCTG | 300 |
| TGATAGAAAT GCCTGCATCC TGAATCCGTT GCAAGAGATC TTCAATCCCA TCAGCGTCCA | 360 |
| AGGTAAAAGG AATAACCAGA CTGCAATTGA TTTCATCATC TGTGCTGTC CCTTTTGTCT | 420 |
| TATGATTACG GATAAATTCT GCTACCTGTA CGTCAAATGT TGTACTTCT TTTGTTTTG | 480 |
| TTGCCATTAT TACTCCATTG TTCTCTTTTG GGAAATTAAA CGTTCCAATT CTCTAGGGC | 540 |
| TGTATCTGTA TCTCCTACAT GGCTAGCTTC CTGCACCTTC TTTTGTATTC CCATATTGTC | 600 |
| CTGATTCAAG AGAGCCTTGT TTCGAAGTCA | 630 |

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

CTAGGGCCAT CTTCTCACCT CCTCCTTGTC AGTACATTCT TGCAATAGAA AAAATAAGAT      60
TGAGTCCCCC CAACCTTAA TTTTTCACC ATCTTCTTTT TCTTTAGCAA TTGCTCTTT      120
GATTTTCTTT TCTTCTTCTT CTTTGC GCGC TTTTCTTCT TCGATACGGC GACGCACTGC      180
TTCACGTTT CCTTCTGGAT CTGGGTGAAT TGTAACGTTT CCTGATTGCA TTTCTTCTAA      240
AGCGCGAAGA GTTGATTTT CAGACTTGAA ACCTTGAGTT GCTGGGGCAC CTGCTTCCAA      300
TTCGTGGGCA CGTTTGTCTT CCAAGATTAC GAGTGAATAT TTTGAAGGAA CCTTGTGCGAG      360
CAAGGTATCA ATAGAGGGT TTAACATCAT TTGCTTGAC CTATTTTCTA AATTTTATCG      420
GGTAGTTGGA GATTTTGGTA ACATCTCCTG ATAGTGACCA ATGACACGAT CCACACAGAA      480
GTGTTCTGCT TCAATCACAC ATTTGACACG TTCAGCAGCT AGGGGTACCT GATCGTTGAC      540
AATCGCATAA TCATACTCAC GCATGAGGGC AATTTCTTCC TTGGCCTTTT CGATTGCTTG      600
GGCAATCACT TCTGCACTAT CTGTTCCACG ACCTACCAAG CGTTCTTGCA ATTCATCCAA      660
ATCTGGTGGT GTCAGGAAGA TAAAGACAGC ATCTGGAACC TTTTCTTGA CCTGAAGAGC      720
ACCTGAACT TCAATTTCAA GGAACATC GATTCCCTTG TCCAAGGTTT CATTGACATA      780
GGTCAGAGGA GTTCCATAGT AGTTGCCGAC ATATTCTGCG TATTCCAACA TCTGTCCTTG      840
ACGAATCAG

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(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

GCCAAACAAC GCATCCATAA TGGTTAAATC TTGATAAGGC AGAGCTACAT TCAAAACAGC      60
TTGCTGGTTT GTAGGCTTTC AATCAGAGCA ATCACTTCTT CAACCTTGTC AGCATCAAGA      120
GCAGCTGTCT CAATCTTTGT ACTTGTTTTC CCTTCCAGTT TAGCTTTCAA GTCATCGCAT      180
TTTGACTTGG TACGGCTAGC AATCATAATC TCTGTAAATG TTTGCTATC TTGACAAATC      240
TTTGAAATAG CAACTTGGGC AACGCCCCCA CAACCAATAA CTAGTAAACG ACTCATTTTT      300
TTCCTTCCTC TTCTTCTAAA ATGTCCTCAA CATACTTGGG CAACATAAAG GCTCCACGT      360
GTAAGTTTGC AGTGTAGTAT TCTGTGAAAA GCTGGCGTTT TTTCCAGCCT TCCTTGTCAA      420
AATCTTTGAC AGGGTGGTAT TTTTTCGATG CAAATCCAAA CAACCAATAG CCAGCTGGGC      480
TAGTTGGAAT ATGGGCCTGA TAAACCCGAC TGATTGGAAG GGCTTGATTG ACCTTGCGGT      540

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GCATGCTTCG GCAGGCCGAC TCATCCTCGT CAAAGAAAGG A

581

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| TTCTGAAAAT | CCATACTTCT | ACCAAGGAGA | TACGCTAGCG | GTCTCGGAAG | TTCTCATACT | 60 |
| TCTATCGCTA | TATCTGGCCA | TCGCCTTTCT | ATCCAAGGAT | TGACAACAAG | AGATAAGGCA | 120 |
| GAGAAAAAAT | TCTTGCTGGA | TCAGCTGGTT | GCCTGCGATG | GTGGTACAGG | TGTCATGCAC | 180 |
| GAAAGCTTCC | ATGTAGATGA | TCCGACCCTC | TACTCTCGTG | AATGGTTCTC | CTGGGCTAAC | 240 |
| ATGATGTTCT | GTGAGTTGGT | CTTGGATTAC | TTGGATATTC | GCTAAGGGGC | TCGCTTTAGC | 300 |
| TCAACCGATT | CTTATCAGAA | TCACAAGTTT | ACATTTAAAA | CGTTAAAATT | TAAATTTAGA | 360 |
| ATGAGGTTTT | ACTTCATGGA | AAATGTTGTT | GTACATATTA | TCTCACATAG | CCACTGGGAT | 420 |
| CGTGAGTGGT | ACTTGCCTTT | TGAAAGCCAT | CGTATGCAAT | TGGTGGAATT | GTTTGACAAT | 480 |
| CTCTTTGATC | TCTTTGAAAA | TGACCCTGAG | TTCAAGAGTT | TCCACTTGGA | TGGACAACT | 540 |
| ATTGTCCTTG | ACGACTAACT | TACAAATTCG | CCCTGAAAAT | CGCGACAAGG | TCCAACGCTA | 600 |
| CATTGACGAG | GGCAAGCTTA | AAATTGGTCC | CTTTTACATC | TTGCAGGATG | ATTATTTGAT | 660 |
| CTCCAGTGAA | GCCAATGTCC | GCAATACCTT | GATTGGTCAA | CAAGAAGCTG | CCAAATGGGG | 720 |
| TAAATCAACC | CAGATTGGCT | ACTTTCCAGA | TACCTTTGGA | AATATGGGAC | AAGCGCCTCA | 780 |
| AATCTTCAA | AAATCAGGCA | TTCACGTGGC | GGCCTTTGGT | CGTGGTGTGA | AGCCGATTGG | 840 |
| ATTTGACAAC | CAAGTCCTTG | AAGATGAGCA | GTTTACGTCT | CAGTTTTCAG | AAATGTACTG | 900 |
| GCAGGGTGTG | GATGGTAGTC | GTGTTTtagg | TATTCTCTTT | GCCAACTGGT | ACAGTAACGG | 960 |
| GAATGAAATT | CCAGTTGACA | AAGATGAGGC | CTTGACCTTC | TGGAAACAAA | AATTGTCAGA | 1020 |
| TGTGCGTTGC | CTACGCTTCG | ACCAACCAAT | GGTTGATGAT | GAAACGGCTG | TGAACACCAG | 1080 |
| CCTGTCCCAA | AAAAAATCTG | AGCGAAGCCA | TTCCGTGTGG | CAAATGAACT | CTTCCCGGAT | 1140 |
| GTAATCTTTG | TTCATAGTTC | TTTTGATGAA | TATGTTCAAG | | | 1180 |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTCAAAAAGT | CTGAAATTGG | ATCATTGGA | ACCATCTGAG | CAGTAAGTTT | AACACCTTTT | 60 |
| TCTGCCAGTT | TGTGGAAGTC | TTCCACATCC | TTGTCTACTA | CGTTGATAGA | ACGTGTAATA | 120 |
| GAACGAGTTT | CTGGTGTTTG | AGACATATTC | CCAACATTAA | GGGTTTCAAG | TGGTACACCT | 180 |
| GCTTCTACCA | AACCAAGGGA | AGCGGTCTGG | TTTACGAGCC | ACGATAAAGA | GACGTTGGCT | 240 |
| ATCGTATTTG | CCAGCAAGAA | TATTGGCTGC | AGCTTTCTCA | ACTGGCAAAA | TACTCAATTT | 300 |
| CACACCTGGT | GGTGTCGCAA | GTTTCAAACC | ACTCTTTTCA | ATATCGTTGT | TGACAACTTC | 360 |
| GTCGTCTACA | ACCATAATGC | GTGAAACATT | TAGTTTTCCA | GCCCAAAGAT | TGGCTACTTG | 420 |
| TCCGTGGATC | AAACGTCCAT | CAATACGGCA | TCCTACAATT | GTCATAAGTT | TTCCCCCTTT | 480 |
| ATATGTTTTA | GTGTAGGTTT | ACGAGTTAAA | TGAATCTCTT | CTTTATATTG | ACCTTCTGTT | 540 |
| TCAAAGATAA | TGATGCGGTT | GGCACCTTCC | TTGAGATAG | | | 579 |

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| CGCATANCCT | AAAAGTTTTT | TTTGACATCT | TCTGGAATAT | CTGTATCATT | AGCTTCCTGA | 60 |
| ACATCTCTAC | CATAAATCCC | AAAGGCTGGA | ATCCCTTTTT | GAGCATGTGA | AGCTAGTACA | 120 |
| GCTGCAAGAT | AGACAGCTCC | TGGGCGTTCT | GTCCCATTA | ATCCCCAAAT | AGCATGAGGA | 180 |
| ATATCTGGAG | ACATATCCAT | AGTTTCACTA | CCATAACACC | AGCATGGTGT | AACTGTAATT | 240 |
| GTTGCGCAAA | CATTTGATTT | TTTAAACAAC | TCATGGGAAG | CTGCAGCCTC | TGGAACACGA | 300 |
| CCAATGGTAG | ATGGAGAAAT | CACACATTCC | ACAGGTTCCC | CATCTGGATA | TTTCAATGTG | 360 |
| CTTGAAATCA | AATCTGCCAC | ACTTTTAGCC | ATGTTTCATTG | TTTGTACTTC | AAGTGATTCTG | 420 |
| CGTACACCTT | GACGACGACC | ATCAATAGTC | GGACGAATCC | CAATACGTGG | ATGTTGAATC | 480 |
| ATACTATTTT | CCTCTTATTT | TTCTGTTTCT | TTCATACTAC | CATCGCCATT | ATATTTACGG | 540 |
| TAGCCTGGGT | GACGACCTGT | AACCTTATAA | TTTTCTCGCA | TTGAGAATAG | ACGTTCTAAA | 600 |
| GTCGGACGAG | CAATTTCTTG | CTCCTCAATG | CCCTTTGTAG | AAAGTAACAT | TCTTCCGTGG | 660 |
| AAGGTTGTCT | TTGCGACTAA | TTCTAAAGTT | TCCATACGGT | AGTATGCTGT | AATTACATCG | 720 |
| CTTCCGACAG | TCAGAG | | | | | 736 |

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

| | |
|--|-----|
| CTCATTGTAT TTAGGAGAAA TGATGGTATC TTCCAAATCA AAATCAACTT CACTCCATAG | 60 |
| TCTCAACGGA TTGATTTTCC CATCTTGATA GGTCAACATCC TTGTCAAGGA TAAACTGAGT | 120 |
| CAACGCCTCA TGCTGACCTT GACACCTGAT GTCATCTACC AAGAGCCAGA CATCCTCTAC | 180 |
| CAACATGAGG ATTTTCTCT TGTGAAGATA AGGCAAATCA GGTTCGTCTG ACCAATAAGC | 240 |
| CCCTTCAATA TAATGCATT CCTCCCTTTC TTTATGGTGA CAAAACAGGG AGTGAGGATA | 300 |
| GTATTCATAT TCCCAGGATC CCGTGATTCT TTCCGGAGCT TTCCCATCTA CAATGCAGGT | 360 |
| CGAATGACTC CAAGCACTCT TTAAGAGATA ACGTTCATAT ATCTCCCGAT AAGAATAACG | 420 |
| CCCAGCATCT ATGAAAATAG GTTGGCCTTG ATACTGTAAG CAAAAACTAT TCTCGTCACT | 480 |
| ATGGCTATGG GCACTTCCTA GCGGACCATT TTTGAAAAAT AGATAACGAT GTTCATCCTT | 540 |
| AATGCAGACA TGTCCAGAGT CTTCAAAGAT CATGGACTTA GGCTGCCAAG | 590 |

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1199 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

| | |
|---|-----|
| CTAGTGTAGC TTCCTTAATC TTATCTGATA AGATAGCTGT CATATCAGAC TCAATCATT | 60 |
| CCTGGAGCAA TCACATTGAC TCGTATATTC CGACTAGCGA CCTCGCGTGC CACAGACTTG | 120 |
| GTAAAGCCAA TCAAGCCAGC CTTAGAAGCA GCATAGTTAG CTTGACCAAT ATTCCCCATC | 180 |
| AAACCAACAA CACTAGACAT ATTAATGATA GCACCTTCTC TGGCTTTCAA TCATCGGTTT | 240 |
| CCAAAGACTG ATTGTGTCAT ATTAAAGGCA CCAGTCAGAT TGACCTTGAG CACTTTTTCA | 300 |
| AAATCTGCTT CTGTCATCTT GAGCATAAGA GTATCTTGGG TAATCCCTGC ATTGTTGACC | 360 |
| AAAACATCTA CTGAACCCAG TTCTGCAATA GCTTGATCAA TCATACGCTT AGCGTCTGCA | 420 |
| AAATCTGATA CATCTCCTGA AATGGGAACC ACCTTGATAC CATAGTTTGA AAACTCAGCG | 480 |
| AGCAATTCTT CTGAGATTGC CCCACGACTG TTTAAGACAA TGTGGCTCC TGCTTGAGCA | 540 |
| AACCTGTGGG CGATGGCAAG ACCAATTCCA CGACTCGAAC CTGTAATAAA GATATTTT | 600 |
| TGTTCTAGTT TCATTTTTTT CCTTTCAAAA CTCTACTTA TTTTAGTCTA TTTTCTAAA | 660 |
| AGTGCYACTA AACTCGCTTG ATCTTCCACA TGAGCTAAGT GAGCAGTTTG ATCAATTTT | 720 |
| TTAACAAAAC CTGACAAGAC TTTCCCGGT CCAATCTCGA ATAAAGTTGC TTATGCCTGC | 780 |

| | | | | | | |
|-------------|------------|------------|-------------|------------|------------|------|
| TTCTTGCAATG | ACCCCAATAC | TTTCATAGAA | ACGAACGGGT | TCCTTGACCT | GACGCGTCAA | 840 |
| GAGCTGAGCA | ATGTCCTCTT | TTTGCATCAC | AGCAGCTTCT | GTATTGCCGA | CTAGGGGACA | 900 |
| AGTAAAATCT | GAAAACTTA | CCTGAGCTAG | AGTTTCAGCT | AGTTTCTGGC | TAGCAGGCTC | 960 |
| AAGGAGAGCG | GTGTGAAAGG | GACCTGACAC | CTTAAGAGGA | ATCAAGCGTT | TGGCACCTGC | 1020 |
| TTCTTGCAAA | AGTTCAACCG | CTCGATCAAC | TGCAACCACT | TCTCCAGCAA | TGACGATTTC | 1080 |
| TGCAGGTGTG | TTATAGTTGG | CTGGAGTAAC | CACTCCAAGT | TCCAGAAGCT | TTTTCAGAGG | 1140 |
| CTTCTTCAAT | GACCTCTACT | GGCGTATTGA | GAAGTGTCTAC | CATCTTGCCA | AGTTCAGCA | 1199 |

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

| | | | | | | |
|-------------|------------|------------|-------------|------------|------------|------|
| CTACTATTTT | CTTTGCCATA | GCCTTCTCCT | TTACACACTA | CGCATATCGT | GGTAAGAAAC | 60 |
| ACTGCGTCCC | ATCTCACCTG | CATTCTCTTT | TTGAACAAAG | GTATTAGCGT | TTATATAGGC | 120 |
| AATAGCAGAA | GCCTTCAACA | CATCAAAATC | AAGCCCTGCT | GCATTAAAGA | TGGTTTCTGT | 180 |
| ATCCCTGTTT | TCAACAGTGA | CCAACAACCC | GATCCTGGGC | ATCGATTCCA | TCTGTTACCG | 240 |
| CATTGATAGT | GTAGGACACC | AAACGAACAG | ATTGGTTAAA | GAAGTTATCG | ATAGCGTTAA | 300 |
| AGATTGCTTC | AACGGAACCC | TGTCCCTGTC | GCATTAAATY | CGACTTTCTC | ACCATCCATA | 360 |
| TTGGCTAGGC | TAACGAGCGC | TTCAATGTCA | TTATCTGCAT | GAGTTTGAAG | TTGTAAATCA | 420 |
| TCAAAGTGGA | AGCCTTCTGG | ATTTTCAACC | ATGGTTCCAG | CTACCAAAGC | TCGAGTATCT | 480 |
| GCATCTGTGA | TTTCTTACTT | CTTATCGGCC | AGTGCCTTGA | ACTTAGCAAA | GAATGGTTTG | 540 |
| ATATCCTCTT | CTGTAAAATC | TAAGGCCAAT | TCTCTCAGTT | TCTCAACAAA | AGCATGGCGA | 600 |
| CCAGATAATT | TTCCAAGCGG | AATCTTAACA | CCAACCAATT | CAGGTGTGAT | GATCTCATAA | 660 |
| GTGAGAGGAT | TTTTAAGGAC | TCCATCTTGG | TGAATACCAG | ATTCGTGGGA | GAAGGTATTG | 720 |
| CCACCAACGA | CGGCTTTGTT | TTTAGGAACT | GGAATACCAG | AGAAGCGAGA | AACCATTTCT | 780 |
| GACGTATTGA | TGGTCTCATT | TAGGACAATA | CTGGTTTCTA | CTTGGTAGTA | ATCTTGGCGA | 840 |
| ATATTGAGAG | CCACTGCAAT | TTCTTCCAAA | GCAGCATTIT | CAGCTCGCTC | CCTAATACCA | 900 |
| TGGATAGTCT | CTTCAAAAAG | TCCTGCACCA | TTCTTGACAG | CAGCAAGGCT | ATTTGCCACT | 960 |
| GCCATCCGAA | GTTCATCATG | ACAGGGAGGC | GAATAGATGA | TCTGACGATC | CGTCTGGACA | 1020 |
| TTCTCAATCA | GGTATTGGAA | GATGGCACCA | CATTCTCTCT | GTGTGGTAAA | TCCTATATTT | 1080 |
| TCTGAAAATT | TCTTCAGTAA | AGAATATTTA | GCTAATTGAA | AGTTCATGAA | AATTATTTAA | 1140 |
| ATATTTTCAAT | TTTTAGAGGT | TAAGTTCCAA | CTTTTTTCTA | TCAATTCCAG | TACTTNTTCA | 1200 |
| TCTGATAAAG | TATCATCAAG | GGACACACTA | ATCCAGTAGC | GCTTGCTCAT | ATGGAAGGCT | 1260 |
| GGATAAATCC | CCTTTTGTGA | AAGCAAATTA | GCTACTTGGT | CATGCTTGAG | GTTGACTGCT | 1320 |
| TCCACTTGTC | CTTCTCTGCC | CTTTTCCAGC | TTATTTCCAAG | AGATTTTCAN | CAAGACGGCA | 1380 |
| TACCACTTTT | GATTGCCTTC | ATGGCGCAAT | ACAG | | | 1414 |

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

CTCCCCATTT TGGAAAATTT CTGTCAAGAA ACGGCGAACC AGCTTTTTTAT TTTCTGCTTT      60
CTTGTCCTAAA TCCTTGATTT CAAAATCTCC AAAAATTTGA TCTAGTTGGT CATTTTCAGG      120
TGTTTCGATAG TAGTCAATGA CATCCCAATG CTCAACAATA CGACCATTCT CATCCGCACG      180
GAAAGTATCC GTCGTCACCC ATTGAGCTTC TCCACCATTG AGATATTGAT GGAACATGAA      240
CAAAGACCAG ATTGCCATCC TCAATGGTGC GGACAATCTT AATCTGACGC TCTGGATGAC      300
GCTCAAAGAA ATCTGCAAAG AAGGCTGCAA ATCCTTCTTT CCCGTCAGGA ACACCTGTCTG      360
AATGTTGGAT ATAGGTATCC CCTACAGACT GGGCTTGAGC CTCAGCAACT CGTCCGTCTT      420
GAATGGCATG GATGTATAGG TTGTGAGCAT TTTTCACTTG TTGTGACATA TTCTAAACCT      480
CATTTCCCTT CTCTTTCAGA TTCGCCAAA TTTCTTCTTG AAAACCTTCA AATTGGTGAA      540
TTTCTTCCTC TGAAAATCCT TTGTAAAAGA TAGTATCCAA TTTCTGACTG ACACGATGCC      600
CCACTTCTTT CTGGGACTTG CCTAACTCCG TTAATACTAA ATACTTCTTA CGCTTGCTCTT      660
TTCCACACGG ACTAACAATT ACAAGCTTTT GTTCCTCTAG CTTTTTTATC ATAGTCGTCA      720
GCGTATTATT CGCAAGCCCA GTCGCAAGCG                                         750

```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

GTATCGTTCA ATTCCAAAGA TACGGAGGAA GCTGCGTTTC GCGAGAAAAC TCTTGTTAGA      60
CCAGATAGGG ATTAGCCAAA ATCCTTCTAT GNGCTTATAT CCAAATGGAG ATGCAAACTT      120
CTGCCCAACT CTTGACCAAT AAGATCTTTC TTAATAATCC ACTCAAGGCT CTGGTAGAGG      180
AAAAATATGG GATTGAGTAT GAAGAATTTA CCAATCCTTG GCACGCTGCC ATTTCTAGCT      240
TCGTTGCCTT TTTCTTAGA AGTTTGCTC CAATGCTGTC AGTGACCATA TTCCCAAGTG      300

```

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| AATATCGCAT | CCCTGCTACT | GTCCTTATTG | TCGGTGTGGC | CCTTCTTCTC | ACTGGTTACA | 360 |
| CTAGTGCCAG | ACTTGGAAAG | GATCCGACTA | GAACAGCTAT | GATTCCGGAAC | CTTGCTATTG | 420 |
| GTCTCTTGAC | CATGGGAGTT | ACCTTCCTGC | TCGAACAAC | TTTCAGCATT | TAGAATACAA | 480 |
| GAAATACCTC | GATTTTGAAG | TCGAGGTATC | TTTTTTACAT | TTGCACAATC | TTGCGATAAC | 540 |
| TTCTTGAAGT | AATCATGAAA | ATCAGCACAT | AGGCGATGAG | GAAGATAGCG | CAGATAGACA | 600 |
| AGGTCACAAT | CAACATCATA | GTCGTATCCA | GTACACCAAT | CACTTTTAAA | ATCAGGCTAA | 660 |
| GCATATGGTA | GGCAAAGGCG | AGATGTATGA | AGGCAAAGAG | CAAAGGAAGG | AAGAAAACAG | 720 |
| TTAAAACCTG | TTTGTGATG | GTTTGCTTGA | TTTGCTTTTG | GTCCAAACCG | ACTTTCTGCA | 780 |
| AGATAATAAA | GCGTTCACGG | TCTTCGTAGC | CTTCAGAAAT | TTGTTTGTAG | TAGATGACCA | 840 |
| GAACAGTTCC | GACCATAAAG | ATAATGGATA | GGAAAATACC | GATAAAGAAG | ACACCGCCAA | 900 |
| AGAGGACACT | CATTTGAGCA | CTAGCATCTG | CTAGATTGCT | ACCATAAACA | TAG | 953 |

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CTGATTGAAC | TTCTATTTAC | TAATATTCAA | AAATCCTCCG | TTTCAAAGAG | CAGGGAAGTC | 60 |
| TTTGTGACAG | AGGATTTTTT | CTATAGGGCT | TTAGCAGCTG | CAATTGCGGC | TTCGAAGTTT | 120 |
| GGCTCAGAAT | TGATATTATC | CACGTATTCA | ACGTAGCGAA | TCGTATTGTC | AGTATCGAGG | 180 |
| ACAAAGACTG | CGCGTGCTAA | TAGGTGCCAT | TCGTTGATCA | AGAGGGCATA | ATCGCGCCCCG | 240 |
| AAAGAATGGT | CAAAGTAGTC | TGAAAGCATA | ATGGCATTGT | CAAGGCCTTC | AGCACC GCAC | 300 |
| CAACGTTTTT | GAGCAAAAGG | TAGGTCCATT | GAAACAGTCA | ATACGACCGT | GTTGTCCAGT | 360 |
| CCAGCCAATT | CTTCATTAAA | ACGACGTGTT | TGAGTTGAGC | AGATGCCTGT | ATCGATAGAA | 420 |
| GGAACGACAC | TCAAGACTTT | TTTCTTGCCA | TCAAAATCAG | CCAGAGATTT | TTTAGAAAGA | 480 |
| TCTGTTGTAG | TAAGAGAAAA | ATCAAGCGCC | TTGTCGCCGA | CTTGTAGTTG | TTTACCTGTA | 540 |
| AAGCTCACAG | GATTTCCGAG | AAAAGTTACC | ATAGGATACT | CCAATCTTTT | TTCTTCCATT | 600 |
| GTATCTGAAA | CAGTCAGAAT | TTTCCAATGA | TTTGACCGGA | AATGTGGGCA | TAGAAAAAAC | 660 |
| GCCAG | | | | | | 665 |

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1039 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

CTAAGTATAA AAAACTTGCC GAAAGTATCT CTGAAGTTAA TTTGAATGTC TTTTTC AAA 60
ATGCTTTAGA TTTTGTGAA ATCTTTAATC AAGAGCCTTG TCTGATAAAT TTTTGTGAGT 120
TTATGAATTC TATGTTACAA GGCGATATTC CAAAGTTAAC AATAAACCAA GAATAATAAG 180
AGGGGAACAG TATGAAAGAT ACGATTTCTA ATAAGGATTT GATTTCATG GGCTATAGAC 240
CATCAACAGC AATGCTATT ATCCATCAGG TGAGAGAATT ACTTGATCA CGAGGCTATA 300
CATTTTATAA TCGCAAACGT TTGATGGTTG TTCCAAAAG TGTGTGAAA GAGTGTGTTG 360
GAATGGAATT GTGAAATGGC TTATATCGAG TATAAACAGC GTGGGAAGAA AAGGCTTTGG 420
TCGTTTTCTA TACGTGAGAG GAGCAAGAGC CTACTCCATA AAAGCGGATT TAAAACAAAA 480
CGAGAAGCTA AAATAGAAGC GGAGAAAGTT CTTCATAAGT TAAATACTGG GAGTGCTTAA 540
AGCTCTAGTA TGACTTTATC GGAGCTTTAT AATGAATGGC TGGATTTAAA AATTTTACCT 600
AGCAATAGAA GTGTAGTTAC TAAAAAATAA TATCTTATGA GAAAGAAGGT CATCGAAAGG 660
TTATTTGGAA ATAAGCCTGT ATCACAATT AAGCCTAGCG AGTATCAAAA AATTATGAAT 720
GAGTATGGAG AGACTGTATC GAGAAATTTC TTAGGAAGAT TGAATTCTAG TATCCAGGCA 780
AGTATACAGA TGGCTATTGC TGATAAGGTG ATAATAGAGG ATTTTACTGC TTATGTTGAG 840
TTGTTCTCTT CTAAGAGTGG ACACAAAGGT TGAGGAAAAG TATCTACATA CTGAGTCAGA 900
TTATCAAAA GTTTTAGTAT ATTTGAAAA TAAGTTTGAT TATCAGAAAT CTATTGTACC 960
GTATGTAATT TATTCCTTT TAAAACCTGG CATGCGTTTC TCCGAATTGA TTGCTCTAAC 1020
TTGGGATGAA GTTGACGAG 1039

```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

CTGAGAAGTC AGGAAGGCGA TGTGGAGAGA TTGAGGAATT GGATACTTAA CTCCATAGTA 60
ATCTTCGTAA AACTCGATAG AGCGAACAGC GATATCCAGT GAGAAATCAA GATTTGAAAG 120
TGGATGTGCT TTGGTTGAGT AGACACCCTA CCAGGGTACC ATTTTATGTT TTAGCGGTCA 180
CCCCTTGCAA ATCACCAGCA ACAAAGGCCA ACAAGTAAGA AGACATGCGA GGTGTTGTCT 240
CAAACCTCCA GATACCTGTT TCCTTACGGT TTCAACATC GATTTCTGGC ATGTTTGACA 300
AGGCCAATTC ACCTTCTGCT TGGTCAAAGC GAAGAGAGAG GTCAAAAGTT GCTTTGGCTT 360
CAGGCTCATC CACACATGGG AAAGCTTCGC GCGCAAAATG GCTCTCGAAC TGAGTAGACA 420
AGACCTCCTT CTTGACTCCA TCAACTGTAT AATAAGAAGG GTAAATCCCT GTCATGTTGT 480

```

| | | | | | | |
|-------------|------------|------------|------------|-------------|-------------|-----|
| CTGTAATTTT | ACCAGAAAAG | GCAAGAACCA | ATTCAACTTG | ACCAGCCTCA | GCCAATTTCGA | 540 |
| TATGAAGGGC | TTCATTGTCA | TGGTCAACTG | TAAATGGACG | AGCTTGACCT | GCAACTTCTA | 600 |
| CAGAGGTGAT | TTCCAAGTCT | TTTTGGTGA | GGGAGATGCG | GTCACCTCTGT | GCTTGACCAG | 660 |
| TGATGGTCAC | TTTCCCAGAA | AAAGTCTTGG | TCTCACGACT | CAAATCTAAA | AATAAATCAT | 720 |
| AATGTTTCAGG | AACAAATTGC | TTAATAAAAT | GTTCAACTGC | TTGCATAGTT | TTCTCCTATT | 780 |
| CTAAGTTTAA | GAG | | | | | 793 |

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGATGATTT | GCTTTTCATC | TATGATAAAG | TCTTTGTTGA | GCGTCGGAAT | CTCTACTGAC | 60 |
| TGGAAATTTT | CCGTAGATAA | TCCAAATGCC | CTTTAAAGAA | AACCTCATCT | GTCAACACCG | 120 |
| AAATCATCAC | TGCTCCGTTT | TCTTCATAAG | TCTGGGCCTG | TTGCACAATA | TCCACATCGA | 180 |
| GATTGATATC | TCCCCAAAAC | TAGGGCTAGC | TTTCTTGACT | TCAGCGATTA | CCTGCAAGCG | 240 |
| GTCCTGATGA | TTCTTCAAAA | ATTCTGCCAA | GCGATAGGTC | TGGCGCAGAG | GCTGGATTTG | 300 |
| CTCCAGCTTC | ATCTGCTCCA | CCTCACGCGC | CTTCTGCTCT | AAGATTCGTG | CTAAAAATTC | 360 |
| CTGACTCATT | TTTGGTACTC | CTGTAACAGT | CTGAGTTTTT | CAAGGGCCTT | GCCTCTAGCA | 420 |
| ATCACTTGAC | GGGCCAAGGC | AACTCCTTCC | TTGATGCTAT | CAATCTTACC | ATTAGCATAG | 480 |
| AAACCAAGAC | CAGCATTCAA | GACTGTCGTT | TCCAAGAATG | GACTTGCTTC | GTTTTTCAGA | 540 |
| ACGCTAAGCA | AAATTTCTGC | ATTTTCCTGA | GCATTCACAC | CACGAATATC | TTCCATAGCA | 600 |
| TAGCCTTCCA | TTCCCAAATC | CTCTGGAGTA | AAGCTTGACA | AG | | 642 |

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|----|
| CTCTTGCAGG | TTATTAAGGA | GAAAACGGAG | GTAATAGAAG | TATGATTTAT | ACAGTCACAC | 60 |
|------------|------------|------------|------------|------------|------------|----|

| | |
|--|-----|
| TCAATCCATC CATTGACTAT ATCGTTCGTT TGGACCAAGT CAAAGTTGGT AGTGTAATC | 120 |
| GTATGGACAG TGATGATAAG TTTGCTGGTG GGAAAGGAAT CAATGTCAGC CGTGTCTTGA | 180 |
| AACGTTTGAA TATATCAAAT ACAGCGACGG GATTTATCGG TGGCTTTACT GGTAAATTTA | 240 |
| NCNCAGATAC TTTAGCAGAG GAAGAAATCG AGACNCGTTT TGTCCAGGTG GCAGAAGATA | 300 |
| CTCGTATCAA TGTTAAAATC NAAGCAGACC AAGAAACAGA AATCAACGGA ACGGGTCCAA | 360 |
| CTGTTGAACC GGTAAAGCTA GAAGAATTGA AAGCTATTTT ATCTAGTCTG ACAGCAGAAG | 420 |
| ATACAGTTGT CTTTGCAGGT TCAAGTGCTA AAAATCTAGG CAATGTTATC TATAAGGGAT | 480 |
| TTAATCTCCT TGACGCGCCA GACTGGTGCG CAAGTGGTCT GTGACTTTGA AGGACAGACC | 540 |
| TTAATTGATA GTTTGGATTA CCACCCTCTT CTTGTAAAAC CAAATAATCA TGAAC TTGGA | 600 |
| GCGATTTTGT GGGTTAAACT CGAAAGTTTA GATGAAATTG AGAAATACGC TCGTGAGTTA | 660 |
| CTGGCTAAGG GTGCTCAAAA TGTTATTATC TCTATGGCTG GTGATGGTGC CCTTCTTGTC | 720 |
| ACATCTGAGG GAG | 733 |

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

| | |
|---|-----|
| CTAAGGGAAG TAGGAAAAGT ATGTATCCAG ATGATAGTTT GACATTGCAA CACGGACTTG | 60 |
| TACCAGATCA ACATGATGCA GGTTTACTTT GATCAAGGGA TTTACAATAA GAAGGCGGTG | 120 |
| TTTGAGGTGT ATTTCCGCCA ACAGCCTTTT AAGAACGGCT ATGCCGTTTT TGCAGGTTTG | 180 |
| GAAAGAATTG TGAAGTATCT TGAAGACTTG CGTTTTTCAG ATAGTGATAT AGCCTATTTG | 240 |
| GAGTCGCTTG GTTATCATGG GCGTTCTTG GATTACCTTC GCAATTTCAA GTTGGAGTTG | 300 |
| ACCGTTCGTT CTGCCAAGA AGGGGATTTG GTTTTTGCTA ATGAACCGAT TGTGCAGGTG | 360 |
| GAAGGACCTC TAGCCCAATG TCAGTTGGTC GAAACGGCTC TTTTGAACAT CGTCAACTAC | 420 |
| CAGACCTTGG TGGCGACGAA GGCAGCCCCC TATCCGTTTG GTTATCGAAA ATGAACCCTT | 480 |
| GATGGAGTTT GGGACACGTC GGGCTCAAGA AATGGATGCG GCCATCTGGG AACACG | 536 |

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| CTGCCCCTGT | AAGGCTGGAC | GATTGCCTTT | CTTAGTATCC | GCAAAGAGGT | AAACTGAGAA | 60 |
| TAGAGAGGAT | TTCTCCTTCA | ATATCTTTGA | CAGACAGGTT | CATCTTGCCT | TCTACGTCTG | 120 |
| AAAAAATCCG | CATATTGACC | AGTTTCTCTCA | CAGCATAGTC | CAAATCTTCC | TCTTGGTCCT | 180 |
| CTGGTCCAAC | ACCAACCAGC | AATAAAAGTC | CCTGATTGAT | TTTCCCTGA | ATCTGGCCTT | 240 |
| CTATACTCAC | TTGGGCTTTT | TTAACCCGTT | GGATAATGAT | TTTCATAATA | GCCTTTCTAG | 300 |
| TAAGAGCTAG | GACAACTAGC | CGTTGGTCCG | TTTGACAGAG | TAAACTTCTG | GCACACTCTT | 360 |
| AATTTTATCG | ACAACCGTGG | TCAGTGTAGA | GAGGTGGCA | ATACCGAAGG | ACACATGGAT | 420 |
| ATTAGCAAAC | TTCATATCCT | TGGTTGGTTG | GGCATTGACC | GTTGAAATAT | TCTTGGTTGT | 480 |
| ATTTGAAAGA | ACTTGCAGTA | CATCGTTCAA | CAGTCCTGTA | CGGTTGAGAC | CGTAGATATC | 540 |
| GATATGGGCC | ATATACTCCT | TATTTGAG | | | | 568 |

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| CTTTATATTG | TACCAAGTAT | CATTTCTAGT | GCTGCTATGG | GCTTGATTTT | TCTTCAAATC | 60 |
| TATAATCCAA | ACTATGGTGT | TGTTAACCAA | ATTATTCATC | TATTTAATCC | ATCGTTTAAA | 120 |
| GATTCACTAC | TGTTGACTCC | CAGGATTAAA | AATAGTAGCT | ATGACTGGCG | CTTATATCTT | 180 |
| CTTTGCAGGA | GCATCAACCA | TTATGATTTC | TTGGGCAAAT | TTTTGCTATT | CCAGAAGAAG | 240 |
| TTCAAGAAGC | TGCTATTTTA | GACAATATTA | CTGGTTGGAG | GAAAGAGTGG | TATATTACGA | 300 |
| TTCCGATGAT | TAAGGGGACA | ATTAAACTG | TTTCAATTAT | GGCAGCAACT | TCAGGATTTT | 360 |
| TGCTCTATAA | CGAAGTATTC | TTTTTGACAA | ATGGTGCTGC | AGGAACAAAA | AGTATCAGTT | 420 |
| TTGTTATTTCG | AGAATTAGCA | GTGGCTAGCT | CACGAACTCA | GTATGCTCGT | GCAAATACAA | 480 |
| TTGGAGTTAT | ACAAATCTTA | GGTGGAATGT | TGATTATCGT | TTGTATTAAT | ATTTTATTCA | 540 |
| GAGAAAGAAA | AAGACTGAAA | GGTGGGAAAT | GATTATGAAT | ACACATATAA | ATGGTATTAG | 600 |
| TAAAAAAGGC | AAAGTTCTTA | TATATGGTTA | TATGCTCCTT | ACCATTTTAA | TTTCTATTTT | 660 |
| CCCTATTGCG | TGGATTTTTT | TATCATCATT | AAAAGCAGAT | CCTATGAAAA | ATCCAGGTAT | 720 |
| TAGTTTACCG | ACTGACTTTA | CTCTTGAAGG | TTATATAAAT | GTTTTTACAA | AACTTCATGT | 780 |
| TTTACTTAC | TTTTGGAATA | | | | | 800 |

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

| | |
|---|-----|
| CTCAGTATTA TCCCTACCAA AATGAACGTC AGTTAGTGAC TCAGGTGGTT TGGGAACAAT | 60 |
| GGGCTTTGGA ATTCCAGCAG CAATCGGTGC TAAAATTGCT AACCCAGATA AGGAAGTAGT | 120 |
| CTTGTTTGTG GGGGATGGTG GTTTCCAAAT GACCAACCAG GAGTTGGCTA TTTTGAATAT | 180 |
| TTACAAGGTG CCAATCAAGG TGGTTATGCT GAACAATCAT TCACTTGGAA TGGTTCGCCA | 240 |
| GTGGCAGGAA TCCTTCTATG AAGGCAGAAC ATCAGAGTCG GTCTTTGATA CCCTTCCTGA | 300 |
| TTTCCAATTG ATGGCGCAGG CTTATGGTAT TAAAACTAT AAGTTTGACA ATCCTGAGAC | 360 |
| CTTGGCTCAA GACCTTGAAG CTACTACTGA GGATGTCCT ATGCTAATTG AGGTAGATAT | 420 |
| TTCTCGTAAG GAACAGGTGT TACCAATGGT ACCGGCTGGT AAGAGTAATC ATGAGATGTT | 480 |
| GGGGGTGAAG TTCCATGCGT AGAATGTTAA CAGCAAACT ACAAATCGT TCAGGAGTAC | 540 |
| TCAATCGCTT TACAGGTGTC CTATCTCGTC GTCAGGTAA TATTGAAAGC ATCTCTGTTG | 600 |
| GAGCAACAGA AGATCCGAAT GTATCGCGTA TCACTATTAT CATTGATGTT GCTTCTCATG | 660 |
| ATGAAGTGA GCAAATCATC AACAG | 686 |

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

| | |
|--|-----|
| TTTTCCAGC TATTTTACTG AGTATAAAAG CCTTATTAA CTTACTCTAT GTACTCGGTT | 60 |
| TTCTAGGAGG AATGTTGGGA GTTGGGATTG CTTTGGGGTA CGGAGTGGCC TTATTGACA | 120 |
| AGGTTCCGGT GCCTCAAACA GAAGAATTGG TGAATCAGGT CAAGGACATC TCTTCTATTT | 180 |
| CACAGATTAC CTATTCGGAC GGGACGGTGA TTGCTTCCAT AGAGAGTGAT TTGTTGCGCA | 240 |
| CTTCTATCTC ATCTGAGCAA ATTTCGGAAA ATCTGAAGAA GGCTATCATT GCGACAGAAG | 300 |
| ATGAACACTT TAAAGAACAT AAGGGTGTAC TACCCAAGGC GGTGATTCTG GCGACCTTGG | 360 |
| GGAAATTGT AGGTTTGGGT TCCTCTAGTG GGGGTCAAC CTGACCCAG CAACTAATTA | 420 |
| AACAGCAGGT GGTGGGGAT GCGCCGACCT TGGCTCGTAA GCGGCAGAA ATTGTGGATG | 480 |
| CTCTTGCCCTT GGAACGCGCC ATGAATAAAG ATGAGATTTT AACGACCTAT CTCAATGTGG | 540 |
| CTCCCTTTGG ATCGAAATAA TAAGGGACAG AATATTGCAG GGGCTCGGCA AGCAGCTGAG | 600 |

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| GGAATTTTCG | GTGTAGATGC | CAGTCAGTTG | ACTGTTCCCTC | AAGCAGCATT | TTTAGCAGGA | 660 |
| CTTCCACAGA | GTCCCATAC | TTACTCTCCT | TATGAAAATA | CTGGGGAATT | GAAGAATTGA | 720 |
| TGAAGACCTA | GAAATTGGCT | TAAGACGGGC | TAAGGCATTC | TTTACAGTAT | GTATCCTACA | 780 |
| GGTGCATTAA | GCAAAGACAA | TT | | | | 802 |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| CTACTATTTT | AGCATAAAAA | TGCCCAAAGG | GGNGCCGTG | TGTTTACTGA | TTTTCAGGNT | 60 |
| AATGGACCAG | GNAAATCAGC | ATGAAAATAA | AAAGAGAAAC | AGATTATTTT | AGCCATTTGT | 120 |
| CAGATTTATG | CTATGCTTAA | GGTAGAAAAT | GAAAGGGATA | ACAAATGTAT | TTAGGAGATT | 180 |
| TGATGGAGAA | AGCCGAGTGT | GGTCAATTTT | CAATCCTTTC | CTTTCTATTA | CAAGAGTCTC | 240 |
| AGACGACCGT | CAAGGCTGTA | ATGGAAGAAA | CAGGATTTTC | AAAAGCAACC | CTAACCAAAT | 300 |
| ATGTCACCCCT | GCTCAATGAC | AAGGCTTTGG | ATAGTGGCTT | AGAACTGACT | ATTCACTCAG | 360 |
| AAGATGAAAA | TCTGCGTCTG | TCTATAGGTG | CAGCTACTAA | GGGGAGAGAT | ATTCCGGAGC | 420 |
| TTGTTTTTTG | GATAGTGCTG | TTAAATACCA | GATTTTGTTT | TATCTTCTCT | ACCACCAACA | 480 |
| GTTTTTAGCC | CATCAGCTGG | CTCAAGAATT | GGTGATTAGC | GAGGCTACGC | TTGGTCGTCA | 540 |
| CTTAG | | | | | | 545 |

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAGGTCAAGA | TTGATTCCCA | AGGTTNGAGG | AATCTGCCGA | ACCAGATTTA | GAAGAAATCG | 60 |
| AGCGGTTACC | ATGCTTGGCC | ATGTGAATAC | CGCCACCAGC | CAAGACAAAG | GCTGCAGTTG | 120 |
| TGGAAATATT | AAAAGTAAAA | GACTTGTCCT | CACCTGTACC | ACAGTTGTCC | ATAGCATCAT | 180 |
| GAATCTCAGT | TGGAATATGC | TGCGCATCTC | CTCTCATGAC | TTGGGCAATG | GCTGTGCGTT | 240 |

| | |
|---|-----|
| CTTCAGGTGT TTCCCCCTTC ATCTTAAGAG CTAAGAGGAG AGAAGCAATC TCGCCTTCAG | 300 |
| TTACACGCCC AGTTACGATA CGCTCAATGA CATCCGTCAT TTCCACACCT GATAAATTTT | 360 |
| CAAATTTTGC TAGTTTTTCA ATAATCTCTT TCATCCTAGT TTCCTCACTT TACAACCTCC | 420 |
| TCGATAAAAT TCCGAATAGA AGACAAGCCG TCTGGCGTTC CAATGCTCTC TGGATGGTAC | 480 |
| TGGAAGCCAT AAATCGGTAG GTTTTTATGT TGAATCCCCA TGATGGCTTG GTCATCAGTC | 540 |
| GAACGAGATC AAGCTTATCG ATACCGTNGA CCTCGA | 576 |

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

| | |
|--|-----|
| ATTAAAGGGA GGCGAACATG GCCCAAGATA TAAAAAATGG AGAAGTAGAA GAAGTTCAAG | 60 |
| AAGAGGAAGT TGTGGAAACA GCTGAAGAAA CAACTCCTGA AAAGTCTGAG TTGGACTTGG | 120 |
| CAAATGAACG TGCAGATGAG TTCGAAAACA AATATTCTTC GCGCTCATGC AGAAATGCAA | 180 |
| AATATCCAAC GCCGTGCCAA TGAAGAACGT CAAAACCTGC AACGTTATCG TAGCCAGGAC | 240 |
| TTGGCAAAAG CAATCTTACC ATCTCTTGAC AACCTTGAGC GTGCACTTGC AGTTGAAGGT | 300 |
| TTGACAGATG ATGTGAAGAA GGGCTTGCGG ATGGTGCAAG AAAGCTTGAT TCACGCTTTG | 360 |
| AAAGAAGAAG GAATTGAAGA AATCGCAGCA GATGGCGAAT TTGACCATAA CTACCATATG | 420 |
| GCCATCCAAA CTCTCCCAGC AGACGATGAC CACCCAGTAG ATACCATCGC CCAAGTCTTT | 480 |
| CAAAAAGGCT ACAAACCTCA TGACCGCATC CTACGCCAG CAATGGTAGT GGTGTATAAC | 540 |
| TAAGATACAA AGCCCGTAAA AAGCTCGCAG TAAAAATAGG AGATTGACGA AGTGTTTCGAT | 600 |
| GAACACAAGA AAATCTANCT TTTTACTCA GAGCTTAGGG CGTGTTTCGAT TCGGCAATTC | 660 |
| TGACGGTAG | 669 |

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTAGTTCACC | ATTTCTATTT | AAATTCGGCT | CAACTACACC | GAAATATCAT | ATAAGGTAAA | 60 |
| GTTCCCACTA | AGAATCTCAG | AATGAAATTC | TTCACCTAAT | TCAGCGGTCA | AACTTAGCTT | 120 |
| ATCCAATTTT | AGACCGATAA | ACCCATACCT | CAGAGATACT | TCCTCTTGAA | ATTTAGAGTA | 180 |
| ACTCTTATTA | GACATTTGAT | GTATCGTTAT | CGGGCTATTA | GAAGGAGCCC | GATTTAAAAC | 240 |
| TTCTTTATTC | ATGAAATTTT | TCCTTCAAAA | AACAAAACAT | TCTATATACT | TAAATTTTAG | 300 |
| GGCAAGACTG | CCGTTCCACT | GACCACGCTC | CACTTGCCAG | CAAAGCTGGC | AGGTCCAGCC | 360 |
| TTACCCTAAA | TATAAATTAT | TTAATTTTGT | CCATTTCAAT | CAATTCTGCA | AAGGTCCCAA | 420 |
| GCTTTCTGGA | TTGAATTACC | TCATATTGGG | CATTCTGTCC | AAATGAAGCA | TTATTAATCA | 480 |
| CTTCAACCTC | ATAAAGGCCT | GGAGCAGAGA | AAACAGCTCC | AAATTTGGAT | TTATCGAAAT | 540 |
| GCATACCTAG | GTCACCTCAA | CAATCATTA | GGGTGGAGAC | TTTATCCAG | CCTCGTTCTT | 600 |
| TCTTAGTAGA | AATAG | | | | | 615 |

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTACTGTAGT | TGGAAGTGT | GAAAAACAAG | GAAAAACAAA | GAAAGTTGTT | ACTTACAAGT | 60 |
| ACAAACCTAA | AAAAGGTAGC | CACCGTAAAC | AAGGTCACCG | TCAACCATAT | ACAAAAGTTG | 120 |
| TCATCAACGC | AATTAACGCT | TAATTTTAAG | GAGAACACAT | GATACAAGCA | GTCTTTGAGA | 180 |
| GAGCCGAAGA | TGGCGAGCTG | AGGAGTGCGG | AAATTACTGG | ACACGCCGAG | AGTGGCGAAT | 240 |
| ACGGCTTAGA | TGTCGTGTGT | GCATCGGTTT | CTACGCTTGC | CATTAACCTT | ATCAATTCTA | 300 |
| TTGAGAAATT | TGCAGGCTAT | GAACCAATCC | TAGAATTAAA | CGAAGATGAA | GGTGGCTATC | 360 |
| TGATGGTTGA | AATACCAAAA | GATCTTCCTT | CACACCAGAG | AGAAATGACC | CAGTTATTCT | 420 |
| TTGAATCATT | TTTCTTAGGT | ATGGCAAAC | TATCGGAGAA | CTCTTCTGAG | TTCGTCCAAA | 480 |
| CCAGAGTTAT | CACAGAAAAC | TAACACGGAG | GAAAACATTA | TGTTAAAAAT | GACTCTTAAC | 540 |
| AACTTGCAAC | TTTTCGCCCA | CAAAAAAGGT | GGAGGTTCTA | CATCAAACGG | ACGTGATTCA | 600 |
| CAAGCGAAAC | GTCTTGGAGC | TAAAGCAGCT | GACGGACAAA | CTGTAACAGG | TGGATCAATC | 660 |
| CTTTACCGTC | AACGTGGTAC | ACACATCTAT | CCAGGTGTAA | ACGTTGGTCG | TGGTGGAGAC | 720 |
| GATACCTTGT | TCGCTAAAGT | TGAAGGCGTA | GTACGCTTTG | AACGTAAAGG | ACG | 773 |

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

| | | | | | | |
|------------|------------|-------------|------------|-------------|------------|-----|
| CTGGATAATT | GGAGCAATTC | CTGATGCCAG | TTTGAGGTTA | CTGATAGGAT | TGTGGGCGAT | 60 |
| AGCCACTTGA | GAAGATGCCA | AGAGTTCAAT | TTCTCTCTCG | TTTAATTCGA | CCCCGTGAGC | 120 |
| AAATACGGAC | GGATGATCTA | AATAACCCAG | TTCTTCAAGA | AAAGCAAGGG | GGCGTTTGCC | 180 |
| GTACCGTTTG | AGGATAATTC | CTGACTCCTC | CTTGGTCTCC | GCCACATGGA | CATGGAGCGG | 240 |
| AATATTTAGC | TCTTTTGCCA | TTTCCAAACT | CGCTTCCAGC | AAGTCTCTAC | TGCAGCTATA | 300 |
| CGGAGAATGA | GGTGCTACCA | TAACCCTTGA | AATTTGGGAT | TTTTATATTT | TAAGATTTCC | 360 |
| TCTATGATGG | ATCGAGTTCT | GCTTATAGTC | TCAGCAGTTG | TTTCTGTCTC | TGAAGAAAAG | 420 |
| AGAGTCGGAG | AAAAATAACA | ACGCATCTTG | GAAGTTTTC | CCACCTGATA | AATTTGCTGG | 480 |
| ATATCCACAC | CATGGGGATT | ATACATATCG | TTAAAGGTTG | TTGTTCTCTGA | CTGGAGCATC | 540 |
| TCTGTTAGGG | CTTCTTTGAC | CGCATTGGTA | GTCATGTCGG | GAGTAAACTC | AGATTCTGCT | 600 |
| GGCCAGATAT | AGTCATTGAG | CCATTTTCATG | GAGATTGCTG | TCATCTCGGA | TCCCTCTCAG | 660 |
| ACCTGTCATT | GCAGAATGGG | TGTGACAATT | GACCAAACCA | GGCATAAGCC | AAG | 713 |

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTAGAAAATC | TGCTTTTTTC | TCGAAAAGTT | TAATACTTGG | TACAATATTA | CGCTTGCTTT | 60 |
| GCTCGGCTGC | TCCAAGGGCA | ATTTTCTCTA | GTTTTTCAAC | TTTTTTACCC | AATTTCTTGC | 120 |
| CATCCCACTT | GGCAACTGAC | CAGTCTGCAG | GAAAGGCCCA | GATTTGGCTA | GCACCCAGTT | 180 |
| CGGTTACTTT | TTGAGCGATG | AACTCCAGCT | TGTCTCCCTT | GGGAAATCCA | GATGCGATGG | 240 |
| TCACTTGGAC | TGGTAGTTCC | ACATTGTCAT | TTAATTCCTG | GACCAACTCA | AACTGACGAT | 300 |
| TTTCCATATC | CAGCACGCGC | GCCAAGCGCT | TGATGCCATC | ATCAAAGACT | AAGGTAACCT | 360 |
| CATCCTCTTC | TTTCAAGCGC | ATAACCTGAA | ACATATGCTT | ACTGGTTTCC | TTGTCCTCGA | 420 |
| TAGTGACAGG | AGAGATAGCA | CTGCCTTTTA | CAAAATACTG | CTGCATGCTA | GCCTCCAATC | 480 |
| ACACCAGAGA | TATCCTTGGT | TTTCTTAAAG | ACACAGGTAT | TCCATTCCCC | TTGAACCATG | 540 |
| TGAGTTTCGA | GGAAAAATCC | AGCTGATTCA | GCCGACTCGC | GCACCATGTC | CCACTTATGC | 600 |
| CTTGAATAAT | GCCACTCATG | ATCAGGTAGC | CTTCGTCCTT | AACCAAACGA | TAGGCATCGT | 660 |
| CTATTAGATG | AATGAGGATA | TCCGCCAAGA | TATTAGCCAC | AATCACATCT | GCCTCAATTT | 720 |
| CCACACCCTT | AAGCAAATCT | CCAGCCGCTA | CATGGATATT | TTCCATGCCA | GGGTTGAG | 778 |

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

CTTCCCAGAT TTTTTCGTTG ACTTGCTGTT CAATCGCACG CAATTCTTCA GCAGTTACAG      60
CTTGGAAGTG GGTAAAGTCA AAGCGAAGGA ATTCAACTTC GTTAAGAGAT CCTGCCTGTG      120
TTGCGTGGTT TCCAAGGATA TTGTGAAGGG CAGCGTGAAG CAAATGAGTC GCAGTGTGGT      180
TTTTCATGAC ACGGTGACGG CGATTGCTAT CAATTGCCAA GGTATATTCT TGGTTCAAGG      240
CAAGCGGTGC AAGGACTTCA ACTGTATGAA GGGCTTGACC ATTTGGGGCT TTCTGAACAT      300
TGGTCACAGT AGCCACAACC TTACCTGACT CATCCAAGAT TTGTCCGTAG TCAGCTACCT      360
GTCCACCCAT TTCAGCATAA AATGACGTTT CCCGCAAAGA TAAGAGAGGC AGTTCCTTCT      420
GAAACAGCTT CTACTTCTGC ATTGTCCGCC ACGAATAGCT ACCAATTTAG AAGACAATTG      480
GCTAGCATTG TAGTTGAAGG CACTTTCTAC AGTGATGTTT TGAAGAGTTT CCATTTTGCA      540
TACCCATTGA GCCACCCTTG ACAGCTGACG CACGCGCGCG TTCTTGTTGT TCTTTCATGG      600
CTGCTTCAAA ACCTTCACGG TCTACAGTCA TACCAGCTTC TTCAGCGATT TCTTCAGTCA      660
ATTCAACTGG GAACCCATAA GTATCATAGA GTTTGAAGAC ATCTGAACCA GCGATAACAG      720
ATTGACCTTT TTCTTTCAAG TCTGCTACAA TGCCTTGGGC AAAGTGTGGA CCTTGAGTGA      780
AGGGTACGGG CAAATGATTC TTCTTCGCCT CTTAACGATT TTCTCAATAA AGTCACGTTT      840
CTCAAGCACT TCTGGGTAGT AGCTTTCCAT GATTTTTCCA ACAGTTGGAA CGAGTTTGTG      900
AAAGGAAAGG CTCGTTGATA CCCAATTTTT GACCCATGCA TAGAAGCACG ACGGAGAAGA      960
CGACGAAAGG ACATAACCAC GACCCTCCAT TTCCTGGAAG GGCACCATCC ACCGATGGCA     1020
AATGAAAGTG AACGGATGTT GGTCCGCGAA TGAACCTTGA AT                                1062

```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

| | |
|--|-----|
| CTCAAAGGTC GCACCTGCAA TACGACCCGC TACAGGACCT ACACCTTGCTC CATGCTTGGG | 60 |
| ACTATTGCCT ACATAACTAC CAAAGTCATC AAATCCCAAG ATAACATTGG CAAAATTTCC | 120 |
| AGCCTTGTC GGTGCGACAT AGCGCAAGAT AGTCGCACCA TAAGTCATAA CCTCAAGTTG | 180 |
| GTAGCCACCG TCTGTCTCAA ATCGATAGGC CAAGACATCC TCACCCCTAA CATTTCCAAA | 240 |
| TACACGCTCT GTGTATGCTT TCATTCTGTT CTCCTTTTAC TATTCTCTC AAGCAAACAA | 300 |
| ACCATAGAAA GCGTACTGAC AATCTATGGT TTATCTGATA ATTTACAAAT CCTCTTGTC | 360 |
| AGAATTCATA AACACTGTCT TACTTTTGAT ATTCTGTAAT TATGACACCT TGTACTACAC | 420 |
| GGTTTACTGT ACCTGTAGGA GACGGTGTAT CTGGTTTATT TTCTACCTTG AGTGAAGTCA | 480 |
| ATAGGGCAAA GAGTTGGGCA TAAACGATGT AAGGGAAGAC ACGGTAAATA TCATTCAAGA | 540 |
| CACCGCCACA ACCAAGGGCC ACTTCTTTGA CATTTTCAAG ACCAAAAGCT TGATCACTCA | 600 |
| AAAGCACAAC ACGACGAGCA ATCTGGTCAC CAGCAACTTC ACGAACCAAG TCCAAGTCGT | 660 |
| ACTTACGAGT GTAGTCCGTC CTTGTACCAA AGAACAAAAC AACTGTATTG TCGTTGATAA | 720 |
| GATATTTGGA CCGTGACGGA ACCAACTGGG CTTTCATACA TGGTCGCAAC TTGAACAACA | 780 |
| GTTAATCCCA AATCTTGAGC TGAGCCTCAT GAGCAGTCCA AAGAAGACCA GCGCCTAGAA | 840 |
| GAGACCGGTT AAGTCTTAAT CACAG | 865 |

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

| | |
|--|-----|
| TTTGTCTCCA GTTGATAAGA AAGGCTTGGT CGATGTTGAG GCGTTAGCAG GTTTGATACG | 60 |
| GCCTGATACA ATCCTCGTTT CCCATCATGG CTGTGAACAA TGAAATCGGC TCTATCCAAC | 120 |
| CNATTGAGGC TATTTAGAA TTCTTGGCAG ACAAGCCGAC TATTTCTTTC CACGTTGATG | 180 |
| CGGTTGAGGC GCTTGCCAAA ATTCCGACTG AAAAGTATCT GACAGAACGG GTGGATTGCG | 240 |
| CGACCTTCTC GAGTCATAAA TTTCATGGTG TCCGTGGTGT TGGCTTTGTC TATATCAAAT | 300 |
| CTGGCAAGAA GATTACACCT CTTCTTACAG GTGGTGGCCA GGAGCGAGAT TATCGTTCGA | 360 |
| CAACTGAAAA TGTGGCAGGG ATTGCAGCGA CAGCCAAGGC TCTCCGTTTA TCTATGGAAA | 420 |
| AGCTAGATAT CTTTAGGAGC AAGACTGGGC AGATGAAGGC AGTGATTAC CAAGCTCTTC | 480 |
| TGAATATCC GGATATTTT GTCTTTTCAG ATGAGGAAGA CTTTGACCT CATATTCTGA | 540 |
| CTTTTGGAAT CAAAGGTGTT CGAGGTGAAG TCATCGTTCA CGCCTTTGAA GACTATGATA | 600 |
| TTTTCATCTC AACCAACCTCA GCTTGTTCAT CTAAGGCAGG AAAACCAGCC GGTACCTTGA | 660 |
| TTGCCATGGG AGTGGACAAA GATAAGGCCA AGTCAGCTGT GCGTCTTAGC CTAGACTTGG | 720 |
| AAAATGATAT GAGTCAGGTC GAGCAGTTT TGACCAAGTT AAAATTGATT TACAATCAAA | 780 |
| CTAGAAAAGT AAGATAGGAG CATTATGCA GTATTGAGAA ATTATGATT GCTACGGAGA | 840 |
| GTTGTCAACC AAGGGTTAAA AACCGTATGC GTTTCATCAA TAACTTCGT AATAATATTT | 900 |
| CGGACGTTT GTCTATCTAT ACCCAAGTTA AGGTAACAGC AGATCG | 946 |

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

CTTGCTCGTA ACAGGTGCTA TCCTTGGTGT CAATGTTTAC ATCTTCTCAC CAAAAGAACT    60
CTTCCCAGAA AAAGAAATCG TTGAATTGGC AGAAGGATTT GCTAAAGAAA GTGGCGCACA    120
TGTTCATCATC ACTGAAGATG CTGATGAAGC AGTTAAAGAT GCAGACGTTT TTTACACAGA    180
CGTTTGGGTA TCAATGGGTG AAGAAGACAA ATTCGCAGAA CGTGTAGCTC TTCTTAAACC    240
TTACCAAGTC AATATGGACT TAGTTAAAAA AGCAGGCAAT GAAAACTTGA TCTTCCTACA    300
CTGCTTGCCA GCATTCCACG ATACTCACAC TGTATTATGGT AAAGACGTTG CTGAAAAATT    360
TGGTGTAGAA GAAATGGAAG TAACAGACGA AGTCTTCCGC AGCAAGTACG CTCGCCACTT    420
CGATCAAGCA GAAAACCGTA TGCACACTAT CAAAGCTGTT ATGGCTGCTA CACTTGGTAA    480
CCTTTATATT CCTAAAGTAT AATTTTAGAT AATAAACCGT CTACCAACAG CTATGAGGGC    540
TGCGACTAAT AG                                     552

```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

CTAAAAAAG TCAAGTAGAA AACGAATATT CTAATTAACT TGCACGAAAT TATTTTTCAC    60
GAATGACTTC GACCTTATAT CCATCAGGGT CTTTGACAAA GTAATAGTTT GGTGCAGTTC    120
CTGGTAGACC ATTTGGCTCA GTCACCTCAT AGCCTTTTGT ACTGTGCTCT TGATGAAGTG    180
CCTCAAGATC AGGTGTACTG AGGGCGATAT GGGCAAACCC ATCACCACCC ACATACGGAC    240
CGTGATCGTA GTTATAAGTC AACTCCAACT CATAGTCATC ACCCTCAAGA CCTAGATAGA    300
CAATCGTGAA GGCATGGTCT GGAAAATCTC TGCGACGCAA TTCTTTAAAA CAAAAGCAT    360
CTTGATAAAA TGCAATTGAT TTTTCAAGAT TTTCTACTCG TAAGCAAGTG TGTAGCATTT    420
TTGAAGCCAT ATCTTTCTCC TTTATTTTAA AAAAGACTGG ACAATCCTGT TCCAGTCTCA    480

```

TCAGTTGTTA TTTACCAAGT TTTGCTTTAG CT

512

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

| | |
|---|-----|
| CTGGACCACA CTATTTTCTG TGTTGGCTAT CGTGTCATGC AAAAGGATCT AGAAGGGACG | 60 |
| CTGGATGCTG AAAAAGCTCAA GGCTGCTGGT GTTCCGTTTCG GCCCGCTTTT TGGTAAAATC | 120 |
| AAAAACGGCC AGGATCTTGT TTTGGAAGAC GGAAGTGAAG TCAAGGCAGC AGACTATATC | 180 |
| TCAGCGCCAC GTCCAGGTAA GATTATCACT ATTTTAGGAG ACGCTCGAAA AACGGATGCC | 240 |
| AGTGTCGCTC TGGCTGTCAA TGCAGATGTC CTAGTTCATG AGTCCACTTA TGGCAAGGGT | 300 |
| GATGAAAAAA TTGCTCGTAA CCATGGTCAC TCAACTAATA TGCAAGCTGC ACAAGTAGCG | 360 |
| GTAGAAGCAG GTGCCAAACG CCTCCTACTC AACCATATCA GTGCCCGTTT CCTCTCAAAA | 420 |
| GATATAAGCA AACTCAAGAA GGACGCTGCC ACAATTTTGT AAAATGTCCA TGTGGTCAAA | 480 |
| GACTTGGAAG AAATGGAAAT CTACCAGTCA CAGAAAGGAT AAGTATGCCT ACTATTCTCC | 540 |
| ATTAACCGGA A | 551 |

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| | |
|---|-----|
| CCGTCATTAT ACCTTTGTCT ATGAAAATGA AGACCTAGTC TATGAGGAGG AAGTCTTATG | 60 |
| ATACAGCCAG CAAGTTTAGA AGAATTAGCA TCTTTAGTGG AAAAAGCGGG CAAGAAGGTC | 120 |
| TTCTTTTGTG TGGCAGACTG GTGTGGCGAT TGTCGTTATA TTTATCCTGC CTTACCAGAG | 180 |
| ATTGAGGAGA CCAATCCAGA GTTCACCTTT ATTCGAATGG ACCGAGATCA GTATATGGAT | 240 |
| TTGGCCAAAC TCTGGGATGT TTACGGAATT CCTAGCCTTG TTGTTCTAGA AAAGGACAAG | 300 |
| GAAATTGGTC GTTTTGTCAA TCGCGACCGT AAAAGTAAGG AGCAAATTAA CGATTTTCTA | 360 |
| GCAGGATTGA AATAGGAGAA AAAGGAAACA ATGATTTTGA CGTATAACAA AGAACATGTC | 420 |

| | |
|--|-----|
| GGTGATGTCC TTATGGTCAT CGTGAAAAAT AGCGGAGATG CCAAAGTAA TGTGGAACGC | 480 |
| AAAGGCAAGG TAGCCCGTGT TTCCTCAAA GAAAATGGGG AACAGTAG | 529 |

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

| | |
|--|-----|
| CTAGGATAGA CCGCTTTTGA GCATTTATCT AAGCATTCCTA GAGTACATGT ATCTTGCATG | 60 |
| TGCTCTTTCT TTTGGGGTTG AAACGATAGG AGAAGGAAAT GTTAGAATTG CTAAATCAA | 120 |
| TCGATGCTTT TGCTTGGGGA CCGCCCTCT TGATTTATTG GTCGGAACAG GGATTTACCT | 180 |
| AACCATGCGG CTAGGACTCT TGCAGGTTT GCGTCTGCCC AAGGCCTTTC AGCTTATTTT | 240 |
| TATCCAGGAT AAGGGACATG GTGATGTATC CAGTTTACA GCTTCTTGTG TAACAGGCCC | 300 |
| TTGGGCATTC AACTGGTTG GGAAACAGGG AAATATCCAT TAGGGAGTTG GCGACGGCTA | 360 |
| TCAAGGTTGG TGGACCAGGA GCTCTATTTT GGATGTGGAT GGCGGCTTTC TTTGGAATGG | 420 |
| CTACCAAGTA TGCGGAAGGA CTCTTGCCA TCAAATACCG CACCAAGGAC GACCATGGTG | 480 |
| CAGTAGCGGG AGGTCCCATG CATTATATCC TTCTAGGGAT GGGAGAAAAG TGGCGACCAC | 540 |
| TTGCTGTTT GTTTGCAGTA GCAGGAGTAT TGGTTGCTCT CTGGGAATC GGAACCTTCA | 600 |
| CCCAAGTCAA CTCGATTACA GAATCTATCC AAAATACAAC GACGATTTCG CCAGCCATCA | 660 |
| CAG | 663 |

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | |
|---|-----|
| CCTTGACCAC CAATCTTCA CCGATATGA TCGCCCTGC TCGTGAGCA AGCCCCAAGA | 60 |
| GATTACTTAT CTTTGCTTA TTCAAGTCCC AACTCTCTC TTTTCACTTT GTGATCCACA | 120 |
| TAAGCGATCA ACTCGTCATA AAAGCTTTCT TCCACTTCCA TGCTAAAGCT GCGGTTAAAG | 180 |
| ACCTTCTTCT TTTTCGCCTC TAGGGCTTCT GCATTGTCTA GTTTGATATA AGCGCCGCGG | 240 |

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| CCATTGGCCT | TGCCCCGTAGG | ATCAATAAAG | ACTTGTCCTT | CCTTGTTCTT | GACAATGCGG | 300 |
| AGCAAATCAC | GCTTATCAAT | CACTTCGTTA | GACACAACAG | ACTTGCGCAA | AGGGATTTTT | 360 |
| CTTGTTTTCA | TCTTTCCCTC | CTCTAGCAGC | TTTTATTCTT | CTACAGTATC | GTTTTCTACT | 420 |
| TCCAACTCTA | CTGAAGCAGC | GTCTTCCATG | GCTTCAAATT | CGCTAGCAGA | CTTGATATCG | 480 |
| ATACGGTAAC | CAGTCAAGTG | AGCCGCCAAG | CGCACGTTTT | GTCCACGACG | ACCAATGGCA | 540 |
| AGAGAAAGCT | TGTTATCTGG | AACAACCACC | AAGGCACGTT | TGCTGTCGTT | TTTCATCAAAG | 600 |
| ATAACTTGGT | CAACCTCAGC | AGGAGCGATG | GCATTGTAGA | TAAATTCAGC | TGGATCTGCT | 660 |
| ACCCACTCGA | TAACATCGAT | ATTTTCTTCG | ATTGGTACCA | TGCGGTCATT | TTTAGCATCG | 720 |
| TAACGAG | | | | | | 727 |

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| CTAATGTAAA | TCTATGGGAT | AAACGTTAGC | TTCTTTTAAT | AGATTATTAA | GCAATTTTTT | 60 |
| AAAACAACCTC | ATCAAACAAA | CTCAACTGGT | TATCTCTGGC | ATATTTCCAA | GAATACCCAT | 120 |
| CTCATCCATC | TTTTCAACCA | AGGTTGATGA | GAGTCCACCA | CGCTTGCGTA | GTTCTGTTTT | 180 |
| AGAGAGGAAT | TCTCCCTCTT | CACGCGCCCG | CACCAGTTGC | TTGGCAACGT | TCTCCCCCAG | 240 |
| ACCATCCATT | GCTACAAATG | GTGGGATAAG | GGTATCCCCG | TCGATGAGGA | ACTCTGTCGT | 300 |
| CTGACTACAG | TAGAGATCTA | ATTTACCAAA | CTTGAAACCT | CGTTCCCA | TCTCATTGAC | 360 |
| AATCTCAAGA | GTGTATAGA | GATCGATTTC | CACATTAGAG | GCTTCATTGT | TCTTCCGTTT | 420 |
| TTCAGAGATT | TCTTCCATTC | TGCGCTTGAT | GACCTCCAAG | CCCGCACCCA | TGGTCTTGAT | 480 |
| ATCAAAAGCC | TTAGCACGAA | TGGAGAAGTA | AGCACAGTAG | TAATAAATAG | GATGGTGAAC | 540 |
| CTTGAAGTAA | GCTACACGCA | AGG | | | | 563 |

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

| | |
|--|-----|
| CTAACTTCAA AAGCTTTTAG AATATCTTCT TGACTAATCA TATGATTACC GCCCAAGGTT | 60 |
| AAGTTTTCCA AAATAGAGCC ATTAAGATA TAGGCTTGTT GGGGTAGGTA ATTAATATGA | 120 |
| CGGCGCAAGA CTTTTTTTAT CAATGTTTTT AATATCCTGA TGATTGATGG AAATATGCCC | 180 |
| TTTGTAGGGT TCAAAGAAAT TGACAATCAT TTTGGCTAAA GTTGTTTTAC CAGAACCACT | 240 |
| AACTCCAACCT AGGCTAACCT TATCTCCTTG TTTAATCGTG AGATTAATAT CTGTTAAGGT | 300 |
| ATCTCGTCCA AAACCATACT TATAAGAAAG GTCATCAAAT TCAATATCGC CCATCAAAAA | 360 |
| ATGTGAATGA ACAGGGTTT CTTGAACTTG AAATTCAGAT TCGACTAGAT AGACTTCGTT | 420 |
| CAAACGGTTA TTAGCGACCT TCGCAGATTG GAGTTTGTT TGGAGGTTGA TAATATTTTC | 480 |
| CATAGGAGTT GTAAAGTAAG AAAGAAGTGT GTTAAAGGTA ATCAGCTGAC CGATAGAAAT | 540 |
| TTTACTCGAC ATGACTAATT GAGCGCCAAA CCATAGGATA AGGATATTCA GAACTAATTT | 600 |
| TGTTTCCCCT GCTTTAACT CGTTTGTAAT ATAGAATATT TACTGAG | 647 |

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

| | |
|--|-----|
| CTATCCTNGA ACCAATGATG CTTGTAACAA TCACTGTTC AGAAGAAAAC CTTGGTGATG | 60 |
| TTATGGGTCA CGTAACTGCT CGTCGTGGAC GTGTAGATGG TATGGAAGCA CACGGTAACA | 120 |
| GCCAAATCGT TCGTGCTTAC GTTCCACTTG CTGAAATGTT CGGTTACGCA ACAGTTCCTC | 180 |
| GTTCTGCATC TCAAGGACGT GGTACATTCA TGATGGTATT TGACCACTAC GAAGATGTAC | 240 |
| CTAAGTCAGT ACAAGAAGAA ATTATTAAGA AAAATAAAGG TGAAGACTAA TCCGTCCTCA | 300 |
| CTCTAGAAGG AAGTCACTTA GTGGCTTCCT TTTGTCTTTA GAAAATACCT CTAAATATGG | 360 |
| TAAAAATAGTA GAAGAATAAT GTGAGGAAAA TGAATGTCAA ATAGTTTTGA AATTTTGATG | 420 |
| AATCAATTGG GGATGCCTGC TGAAATGAGA CAGGCTCCTG CTTTAGCACA GGCTAATATT | 480 |
| GAGCGAGTTG TGGTTCATAA AATTAGTAAG GTATGGGAGT TTCATTTCCG TATTTTCTAA | 540 |
| TATTTACCTA TTGAAATCCT TTTTACAATT AAAGAAAGTT TGAGCGAAGA ATTTCTTNAG | 600 |
| AANGCCATCA | 610 |

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TATAAGCATA | GTACCAGTTG | CCATTGACCT | GGAACCAACT | GTCTTCATAT | CTCCATTACT | 60 |
| GCATTTAGGT | AGTACCAAGT | TGAACCATCT | TGATACCAAC | CAGTTGCCAT | TGCTCCTGAT | 120 |
| GAACGGAGAT | AGTACCATTT | GTTCCCAAGG | TTTTGCCAAC | CTGTTTTCAT | ATCGCCATTT | 180 |
| GGCTGGTCTA | AATAATACCA | AGTGGTACCT | TCCTGATACC | AACCAGTTGC | CATTGCTCCT | 240 |
| GATGAACGGA | GATAGTACCA | TTTGTTCCCA | AGGTTTTGCC | AACCTGTTTT | CATATCGCCA | 300 |
| TTTGGCTGGT | CTAAATAATA | CCAAGTGGTA | CCTTCCTGAT | ACCAGCCAGT | GGCCATTGCT | 360 |
| CCTGAGGAAC | GGAGGTAGTA | CCACTTATTA | CCTAGATATT | GCCAACCTGT | TGTCATAATA | 420 |
| CCAGTTGTTG | GATCTAAATA | GTACCAAGTC | AAATCATCGT | TTATCCACCC | CGCACGCTTT | 480 |
| TCACCACCAA | GGTAGTTTTC | TCCATTAAAT | TCCGTCCTAG | CTAGATAATA | CCAGTAGACT | 540 |
| GATCATAAAG | CCAACCTGTC | TCTAAAGAAT | GATTTTGATT | AAAGTAATAG | TTCGTATAAT | 600 |
| AACGNTTCTC | TTCTTTATCT | TCTGAATCTT | CACGTTTTTC | CCCGTACTTT | CTTCCAACAC | 660 |
| TGTCTTTAGT | TTTAATCTCT | AATGTTTTCC | AACCAACAAA | CTCTTGTAGC | ACTCCATTTT | 720 |
| TATCGAAGTA | GTACCACTCT | GAATTTGGAA | AACCTTCTAA | TCTCATACCA | TTTGGGTAAG | 780 |
| GACCAATTGT | ACTACCTTTA | GATGGAAACG | GGATATATG | CCAGCCGACA | ACCATCTCTC | 840 |
| CAGATAGAGA | ATCAAAATAA | TAGTACTTAC | CATCAATCAC | TCGCCAGTAG | GTTTCTTTGA | 900 |
| GGTCCCCCTT | TTTGTAATAG | GTTCTACCGT | TTTCTTGGAC | AAACTGCCAT | CCTTCAGAGT | 960 |
| TATCTGCAAA | TACTGTATTC | GTAG | | | | 984 |

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 842 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCTCGTTATG | CAGATGAACG | TTATTTCTTG | TCAAAGAGTC | ACAAGAATTT | TGTTGATCGT | 60 |
| AATCTTTTTA | TTACCATTCG | TGACAAGGAA | ACCACCTGTA | TCAAGCCTTA | TCAGCAGGAT | 120 |
| TTGGATTTGC | CACATGGTCT | GGCCTTGGAT | GTTTTGCCTT | TGGATTATTA | TCCGAAAAAT | 180 |
| CCAGCTGAGC | GGAAAAACN | GGTTCGTTGA | GCCTTGATTT | ATTCACCTTT | TTGTGCGCAA | 240 |
| ACTATTCCAG | AAAAGCATGG | TGCTCTCATG | AAATGGGGAA | GTCCGATTTT | ACTGGGTTTG | 300 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTCCAAAAT | CTCTCCGTTA | TCGCATCTGG | AAAAAAGCTG | AGAAAGAAAT | GACTAAGTAT | 360 |
| GATTTGGCTG | ATTGTGATGG | CATTACAGAA | TTATGCTCAG | GTCCTGGCTA | CATGAGAAAC | 420 |
| AAGTACCCAA | TCACATCTTT | TGAAGACAAT | CTTTTCTTGC | CATTTGAAGG | AACAGAGATG | 480 |
| CCTATTCCAA | TCGGCTATGA | TGTCTATCTC | AGAACTGCTT | TTGGGGATTA | TATGACGCCT | 540 |
| CCACCAGCAG | ACAAGCAGGT | ACCGCATCAG | GATGCTGTCA | TCGCTGATAT | GGATAAGTCT | 600 |
| TATACAGAAT | ACAAGGGAGA | ATATGGTGGC | TAAGAAAAAA | ATCTTATTTT | TTATGTGGTC | 660 |
| TTTTTCTCTT | GGAGGTGGTG | CAGAGAAGAT | TCTATCAACC | ATTGTTTCAA | ATCTGGATCC | 720 |
| AGAAAAGTAT | GATATTGATA | TTNTTGAAAT | GGAGCACTTT | GACAAGGGAT | ATGAATCTGT | 780 |
| TCCAAAGCAT | GTACGCATTT | TAAATCCCT | TCAAGATTAT | CGCCAAACCA | GATGGATACG | 840 |
| AG | | | | | | 842 |

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGGCAAATA | CAAGGTGACG | ATCATTGGTA | AATCAGCCCA | CGGTGCTATG | CCTGCTTCAG | 60 |
| GTGTCAATGG | TGCGACTTAC | CTAGCCCTCT | TCCTTAGCCA | GTTTGACTTT | GCTGGTCCAG | 120 |
| CCAAAGAATA | CCTTGACATC | ACTGGTAAAA | TTCTCTTGAA | CGACCATGAG | GGTGAAAGTC | 180 |
| TCAAGATTGC | TCATGTGGAT | GAAAAGATGG | GTGCCCTTTC | TATGAATGCA | GGCGTCTTCC | 240 |
| GCTTCGATGA | AACAAGTGCT | GATAATACCA | TTGCCCTCAA | CATCCGCTAT | CCAAAAGGAA | 300 |
| CAAGTCCAGA | ACAAATCAAG | TCAATCCTTG | AAAACCTTGC | AGTTGTTTCT | GTTAGCCTGT | 360 |
| CTGAACACGG | TCACACGCCT | CACATGTGTG | CCAATGGAAG | AATCCACTTG | GTTGCAAAAC | 420 |
| TGGTTGAAAT | GTCTATGAAA | AACAGACAGG | CCTTAAAGGT | CATGAACAAG | TCATCGGTGG | 480 |
| TGGAACCTTT | GGTCGCTTGT | TAGAGCGCGG | AGTTGCCTAT | GGTGCTATGT | TCCCAGACTC | 540 |
| AATTGATACC | ATGCACCAAG | CCAATGAATT | TATTGCCTTG | GATGATCTCT | TCCGAGCAGC | 600 |
| AGCAATTTAT | GCCGAAGCTA | TTTACGAATT | GATCAAATAA | AACGATAGAA | GTCTGAGATC | 660 |
| TTATGCTTGG | ACTTCTTTTT | GGAGGGAAAG | TAGATGTCTC | AAATCGAAAG | AATCAAACAG | 720 |
| GCTATCATGG | CGGATTCACA | GAATGCCAG | | | | 749 |

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGGATGAAT | TGCAGAAGCG | CAACCTACTG | GGATTTGTCT | TCCAAGATTT | TCAACTATTT | 60 |
| CCTCATCTAT | CAGTTCTGGA | AAATTTGACT | TTATCGCCTG | TGAAGACCAT | GGGAATGAAG | 120 |
| CAGGAAGAGG | CTGAGAAGAA | GGCGAGTGA | CTCTTGAAC | AGTTAGGACT | AGGAGGACAC | 180 |
| GCAGAGTCCT | ATCCTTTCTC | ACTATCTGGT | GGGCAAAAGC | AGCGGGTGGC | TTTGGCGCGT | 240 |
| GCTATGATGA | TTGACCCAGA | AATCATTGGC | TACGATGAAC | CAACTTCTGC | CCTGGATCCA | 300 |
| GAATTACGTT | TGGAAGTGA | GAAGCTAATC | TTGCAAAATA | GGGAAGTTGG | GATGACCCAC | 360 |
| ATTGTGGTTA | CCCATGATTT | GCAGTTTGGC | TGAAATATC | GCACATGTTA | TTATTGAAAG | 420 |
| TAGAACCTCA | AATAGGAAGA | AAAATGGATT | GAAGAAATGG | ATGCTTGTAT | TAGTCAGTCT | 480 |
| GAAGACTGCC | TTGTTCTTA | GTA | | | | 503 |

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGGAGGGCA | TTCAGTATTA | CTTGAATAGA | GGAAAACATC | ATCTCCCTTA | TGTTCTCAAT | 60 |
| ATTGGATTTC | CTGGTCAGAA | AAATGACCTC | TTACTCCTTC | GGCTAGATTT | AGCTGGAATT | 120 |
| TCAATCTCTA | CTGGCTCAGC | CTGTACTGCA | GGCGTTGTCC | AATCCAGCCA | TGTTCTTAAA | 180 |
| GCCATGTATG | GCGCAAATTC | AGAACGCTTG | AAGGAATCCC | TTGCGATCAG | TTGTGCGCCA | 240 |
| CAAAATACCG | TTGAAGACCT | ACAAACCCCT | GCAAAAACCT | TAAAAGAAAT | TATCGGAGGT | 300 |
| TAGCCATATG | GCATTTGAAA | AAATCATTCA | GTAAAAAAT | TGTCGTTACG | ATTACACTCT | 360 |
| TAGCCCTTCT | GTAAAAAAT | TCACCCCTCA | AGATAACACC | TTTTTTGAAA | CTAAGGTTGG | 420 |
| TAAGTATGAA | CTGACTCGCC | TTTTGGAAAA | AGTGCCAAAC | AGCGGTGAAG | GCTTCCAAC | 480 |
| CAAAATCATC | ATTAACAAGG | AACCTACAGG | GGCTAAAATC | AATATCACTG | ACAAGTTTGG | 540 |
| CCTTCGTCTA | GTGATATTT | TCAAATCAGA | AGACCACCAT | ATTCATCAGG | AAAAATTCTA | 600 |
| CTTCCTCATG | GATAG | | | | | 615 |

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

| | |
|---|-----|
| CTGCAATGGT TAGCGAGGAT GGTGAAATAG AGGAGCCTTA ACTATTTTGA GGAATCCAAG | 60 |
| CTGACAGGAC TGGTATGTCT GCTCTTTGGC TCTGAAGGCA GACTATACCA GCTGGAAGTT | 120 |
| TGACAGATGT GGCACGTGAG AATTATTGGA GGCNTTGACN TANTCAGAGG ATTCTCTCTT | 180 |
| GATATTGGGT TTGGCAGAGT TGGATAGTGA GTTGGAAAAT TACCAAGCGG TTATTCAAGC | 240 |
| CTATGCCCAG TTAGATAATC GCTCGATTTA TGAGCAAACG GGCATTTCCA CCTATCAACG | 300 |
| AATTGGCTTT GCCTATGCTC AGTTAGGGAA ATTTGAAACG GCTACTGAGT TTTTAGAAAA | 360 |
| AGCCCTGGAG TTAGAATACG ATGACTTAAC AGCTTTTGAG TTGGCCAGTC TTTATTTTGA | 420 |
| TCAAGAAGAA TATCAAAAAG CCACCCTCTA CTTTAAGCAG CTTGATACCA TTTCTCCTGA | 480 |
| CTTTGAAGGC TATGAGTATG GGTACAGTCA GGCTTTACAT AAGGAACATC AAGTTCAAGA | 540 |
| AGCCCTGCGT ATCGCTAAGC AAGGATTAGA GAAAAATCCC TTTGAAACTC GCCTCTTGCT | 600 |
| AGCTGCTTCA CAATTTTCTT ATGAATTGCA TGATGCTAGT GGTGCAGAAA ATTATCTCCT | 660 |
| TACTGCAAAA GAAGACGCTG AGGATACAGA AGAAATCTTG CTTCGTTTAG CCACTATTTA | 720 |
| TCTGGAGCAG GAGCGTTATG AGGATATTCT AGACTTGCA AGTGAGGAGC CAGAAAATCT | 780 |
| TTTGACCAAG TGGATGATTG CTCGTTCTTA TCAAGAAATG GACGATTGG ATACTGCTTA | 840 |
| TGAGCATTAT CAAGAGTTGA CAGGAGATT GAAGGACAAT CCAGAAATTC TGGAAACATA | 900 |
| TATCTATCTC TTGCGTTGAA TTGGGACATT TTGAAGAAGC AAAATCCCAT GCTC | 954 |

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

| | |
|---|-----|
| CTATGAAACA TTTTGATACT ATTGTCATCG GTGGGGGACC TGCTGGTATG ATGGCTACGA | 60 |
| TTTCCAGTAG CTTTATGGA CAGAAAACCC TCCTCATCGA AAAAAATCGG AAACCTGGAA | 120 |
| AAAAATTAGC TGGGACTGGT GGGGGACSTT GCAATGTGAC CAACAATGGT AGCTTAGACA | 180 |
| ACCTGCTAGC TGAATTCCT GGAAACGGAC GCTTCTTTA CAGTGTTTTC TCCAGTTTCG | 240 |
| ATAATCATGA CATCATCAAC TTTTTTACAG AAAATGGTGT TAAACTTAAG GTCGAAGACC | 300 |
| ACGGACGCGT CTTTCCAGCC AGTGACAAGT CTCGGACTAT TATCGAAGCT TTGGAAAAGA | 360 |
| AAATCACTGA ACTAGGTGGT CAAGTTGCTA CTCCAAATAG AAATCGTTTC TGTAAAAAA | 420 |
| GTAGATGACC AGTTTGTCTT TAAGTCAGCG GATCAAACCT TCACTTGTGA GAACTCATT | 480 |

GTCACAACAG GTGGTAAGTC TTATCCTTCG ACTGGTTCGA CTGGTTTGG TCACAATGCT 540
 CCGCCATTTA AGCATACCAT CACG 564

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTCCGTGGTC TTTTGGTTTG CTACGGGATG TAGGCAAAAG GCAAGTCCAT TTTATCAGCA 60
 ATAATGGCTC CGTGTGGAAT CCCTGCTGTT GCAGTTCCTG CAATCACTTC TACTTCAGGA 120
 AAGGCTTCTT TGATAGCTTC CACAAAACCA TTTTCAATTA GGGTACGAGT TTCTGGATAG 180
 GCTAGTGTC CACGATTATC AGTGTAATC GGTGACTTGA TACCAGATGC CCAAGTGAAG 240
 GGTTCCTCTG GTTTGAGGTA AACGGCTTGG ATTTTCAAGA GGTGGCTAGC GATATCTTTA 300
 GCAAGTGTC TGGTATTCTC CTTTTATTTT TCTAATCTAG TTCTTTAATT CCAGTCCTGT 360
 GTCCATTCAT CCTGATGGC ATGATAAGCT GCAACAGGAT CCTCAGCTTG GGTAAATGGGA 420
 CGTCCCCTA CGATATAGTC ACTGCCGATT TGATAGGCAT CAGCAGGTGT CATGACTCGT 480
 TTTTGATCTC CAACTGCAAC ACCAGCTGGA CCAATCCCTG GTGTCCCGAC AGATAAAAAT 540
 CTGGATTGGT AGCCCTGCTT GATGACTTTG TCACTTCCCT GAGCCGAGCC AAACCAACAC 600
 CCATCCCAAA GCCCAAGCTT CAGCTGTCTT CCTTGGCATA GTTGAATCCA C 651

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CTTAGTATCT AGAAAAGGAG AAATAAAATG GTTAAAGTAT TAGCAGCGTG CGGAAATGGA 60
 ATGGGTTTCAT CAATGGTTAT CAAGATGAAG GTTGAAAATG CTCTCCGTAA GCTTAATCAA 120
 ACAGATTTTA CAGTCAATTC ATGCAGTCTC GGTGAAGCTA AAGGTTTAGC AGTAGGATAT 180
 GACATCGTAA TCGCTTCTCT TCATTGTATT CAAGAATTGG AAGGGCGAAC TAATGGGAAG 240
 TTAATTGGGC TTGATAACTT GATGGATGAT AAAGAAATCA CCGAAAACT CAGTCAAGCA 300

| | |
|---|-----|
| ATACAGTAAA AGGTTGGAGG GGGCTGGACA CAAACTGAGA GTTATCGTTT CTGTCCTTCT | 360 |
| CCCTCTTTAA ATAAAGGAGG CAGATATGAA TTTAAACAA GCTTTAATTG ACAACGACTC | 420 |
| GATCCGACTA GGTTTAGAAG CTAACGAATG GAAAGAAGCA GTCAAGGTAG CAGTAGATCC | 480 |
| CTTGATTGAA AGTGGGGCAA TTTTGCCAGA GTATTACGAT GCTATCATTG AATCGACTGA | 540 |
| AGAGTATGGG CCTTACTATA TCTTGATGCC AGGTATGGCT ATGCCCCACG CTAGACCTGA | 600 |
| AG | 602 |

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

| | |
|--|-----|
| ATTGGGAATT TTTGCAACTG CAATTGGTGC CCTCAGTAAT CTATAAAATA GATTCAAGAA | 60 |
| AATTTAGTGA CTGGGATTTC CCAGCCCTTT TTTAAAGTGA GAAGAAATAA TGAGTATGTT | 120 |
| TTTAGATACA GCTAAGATTA AGGTCAAGGC TGGTAATGGT GGCGATGGTA TGTTGCCTT | 180 |
| TCGTCGTGAA AAATATGTCC CTAATGGAGG CCCTTGGGGT GGTGATGGTG GTCGTGGAGG | 240 |
| CAATGTGGTC TTCGTTGTAG ACGAAGGACT ACGTACCTTG ATGGATTTCG GCTACAATCG | 300 |
| TCATTTCAAG GCTGATTCTG GTGAAAAAGG GATGACCAA GGGATGCATG GTCGTGGTGC | 360 |
| TGAGGACCTT AGAGTTCGAG TACCACAAGG TACGACTGTT CGTGATGCGG AGACTGGCAA | 420 |
| GGTTTAAACA GATTTGATTG AACATGGGCA AGAATTTATC GTTGCCCCACG GTGGTCCGTG | 480 |
| GTGGACGTGG AAATATTCGT TTCGCGACAC CAAAAATCC TGCACCGGAA ATCTCTGAAA | 540 |
| ATGGAGAACC AGGTTCAAGG ACGTGAGTTT ACAATTGGAA CTTAAA | 586 |

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

| | |
|---|-----|
| TTCGACAATC TTGCCCNGA TCCAAGACAA CCACTTCTCT GTCCGCTCAG CAATAGTCAA | 60 |
| GCGGTGAGCA ATGAAAATCA AAGGTCTTCT CCAAAGCCAT GAGATAATGG ACAATCCGTT | 120 |

| | | | | | | | |
|------------|------------|------------|------------|------------|------------|-------------|-----|
| TTTTTGTC | AAATATCC | AAATATCC | CTGTAGTC | CCTCATCC | AAATCAAG | GGCGCATCTG | 180 |
| TCAAGAGAG | ACGCGCCAA | ACGCGCCAA | GCGATTCT | GACGTTGACC | ACCTGAAATC | CCTGCCCCAT | 240 |
| CCGAAGTCA | TTCTGTCT | TTCTGTCT | TAAATTTCA | GGTGGCATGG | CGGCTTCGAG | ATATTCCCTCT | 300 |
| TCGGAATCTC | TGAACCAAAT | TGAACCAAAT | TCGGACCGGC | CCGTAAAGA | TATCTTCCCT | GTGTCGTCCC | 360 |
| CTCCCTTGGC | TCCCAAAGA | TCCCAAAGA | AGATTCTCCA | AAATCGTTCC | GTTAAAGACA | TAGGGCTGTG | 420 |
| GAGGCAGATA | GATGATGTAC | GATGATGTAC | TGGCGTAGGG | CTTTTTTATC | AATCTGATTG | AGATTGACAC | 480 |
| CACCCAGACT | AATCTCCCTT | AATCTCCCTT | TGACTTGGGT | CGTAAAAATT | AACCATCATC | TTGGCCAAAG | 540 |
| TCGTCTTACC | TGACCCTGAA | TGACCCTGAA | ATCCCCACAA | AAGCCACCTT | AGACCCTTGG | GGAACGGTTA | 600 |
| AATTGATATC | CGACAAGACG | CGACAAGACG | TCTCGACCAT | AGCCATACTT | GTAATGAACC | TGCTTGAAAG | 660 |
| TCATCTCTCC | CTTCATCAAG | CTTCATCAAG | | | | | 680 |

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCAATTTGGA | TTTGCAGAA | GGCGTTATTA | TTTCAGATGC | TGGTTCGACC | AAGTCAACCA | 60 |
| TTGTGGATGC | GGCGGAGCAG | TATTTGGCTG | GCAAGTCTGT | TCGCTTTGTC | GGGGCCCATC | 120 |
| CCATGGCTGG | TAGTCACAAG | ACAGGGGCTG | CTTCGGCAGA | TGTCAATCTT | TTTGAAAATG | 180 |
| CCTATTATAT | CTTTACAACC | TTCCAAAGCC | CTGAACAAGT | CAAGGACAAC | GCTTAAAGGA | 240 |
| AATGGGAAAG | GATCTGCTTT | CCAGGTCTTC | ATGGCTCGTT | TTATCGAGAT | TGATGCCAAG | 300 |
| GAGCATGATC | GTGTCACTTC | TCAGATTAGC | CATTTTCCTC | ATATTTTGGC | TTCTAGTCTC | 360 |
| ATGGAGCAGA | CTGCGGTCTA | TGCTCAAGAG | CATGAGAATG | GCAAGGCGCT | TTGCGGCAGG | 420 |
| TGGTTTTCGA | GATATGACCC | GAATTGCGGA | AAGCGAGCCA | GGAATGTGGA | CCTCCATTCT | 480 |
| CTTGTCGAAT | AGCGAGACCA | TTCTGGATAG | AATTGAGGAT | TTCAAGGAAC | GTTTGGAAGC | 540 |
| GATTGGTCAG | GCCATTAGTA | AGGGAGATGA | AGAGCAAATT | TGGAACTTT | TTAACCAAGC | 600 |
| G | | | | | | 601 |

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGGCTCATC | AGGGGCAGGA | TATTTATGAT | TTCCCTCGTG | CTATGATTAA | GGAAGATAAT | 60 |
| CTGGAGTTTT | CATTCTCTGG | TTTGAAATCT | GCCTTTATCA | ATCTTCACCA | CAATGCCGAG | 120 |
| CAAAGGGGAG | AAAGTCTGTC | TACAGAGGAT | TTGTGTGCTT | CCTTCCAAGC | AGCTGTACTG | 180 |
| GATATTCTCA | TGGCAAAAAC | CAAGAAGGCT | TTGGAGAAAT | ATCCTGTAA | AACCCTGGTT | 240 |
| GTGGCAGGTG | GTGTGGCAGC | CAATAAAGGT | CTCAGAGAAC | GCCTAGCAGC | CGAGGTTACA | 300 |
| GATGTCAAGG | TCATCATGCC | ACCTCTGCGC | CTCTGCGGAG | ACAATGCAGG | TATGATTGCT | 360 |
| TATGCCAGTG | TCAGCGAGTG | GAACAAAGAA | AACTTTGCAA | ACTTGGACCT | CAATGCCAAA | 420 |
| CCAAGCCTCG | CTTTGATAC | CATGGAATAA | AGAGTGGCTC | TTGTCAAGT | GTAGTGGGTA | 480 |
| GGCGAAAAGC | TACAATCTGG | AGANTACGAA | ATTG | | | 514 |

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| CTTGGATTAT | AAAATACAAT | CGGCAAGATC | ATAAGTCCCA | AGCCTAAAAA | TATATAGAAA | 60 |
| GGGGGTCACC | TTCCAAAGAA | ATTCTGTATT | AAAGAGCATG | ACCACAAAAC | CAATCACAAG | 120 |
| CCCCAAGGCA | ATCCAGGCGA | CCTGCTGCCC | TAAAATGGGC | AGAATATTAT | TGGGGTAATC | 180 |
| ATGACTAACG | GCTATATAGA | TAGCCACCAC | ACCGATGACC | AGTAGAAAAA | ATACTGGCAA | 240 |
| GAGCAAACCTG | TAATCGACTC | TTGAGTCGAG | AGAACGTTTC | ATATAAACTA | ACCTTATACT | 300 |
| TTCATACAAT | ACTATTTATC | AAAGTTCATT | AAAAAATCTA | TCAATAGCCT | CGTCAACTTC | 360 |
| GGATCGAGAG | ATGGTTTTAA | CAGTCGCTTC | TTCTGCTAGA | GATGCTACTA | TTTGTGTTGCC | 420 |
| GTATCGTTTT | CCGACGATTC | TCCTATCCAA | AATAAGAGTT | AAGGAACGTT | GGTATTCACG | 480 |
| TCTCATACTT | CTTCCCAAAG | CCTGTTTTAA | ACGAATAATG | G | | 521 |

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CTTGCGTGAT | GACATCATTG | ACTCTTTTTG | GTATATCATC | GACCATTCT | TAAAAAATGT | 60 |
| CTTTGAATTG | GAAGAAGAAC | TCGAGTTTCA | ATTGCTTAAT | AACCAAGGAA | AGATTACCTT | 120 |
| CCACTTTTCA | AGTCAACACC | TCCCTACAGC | CATTGATTTT | GACTTTAACC | ATCCTTTTCA | 180 |
| CCCTCGTTAT | CCCCCAAGAG | TACTGGTTTT | AGACATGGAC | GGTAGAGAAA | CTATCCTCCT | 240 |
| CCCAGAAGAA | AATGACCTAT | TTAAAAACT | CTAGCCTTCA | GTTGCAAGTG | ACTGAAAACT | 300 |
| AGAGTTTTTC | TATTTTTTCA | AAGCATCATA | CAAGTTGCGG | ATCGGTTGTT | TTAATATCGG | 360 |
| ATGGATAAAA | TGAGGCGCAA | TTTCTGTAA | GGACTCAAGG | ACAAAAAGGC | GTTCCCGCTA | 420 |
| TGTTAAGGGA | TGAGGCAATA | TGAGGTCGTC | TGTATAAAGG | ATCTGGTCCT | CCCACAAAGA | 480 |
| GCAAGTCCCA | AATCAATCCA | AACGAAGTCC | CCCAATGCAC | TTCTCTCACC | CGTCCCCCAGC | 540 |
| TCTTGACTCC | AATGGCTAAC | AAGGTTTCNT | AACAATTCTT | GTTGCTGGTA | GCCAAGTTC | 599 |

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| CTATGGGTAA | AAAGGATGCC | TCTGCTATGC | ATGAGATGAG | GGCTTCCTTT | ATTCAAGGCT | 60 |
| CCATAGAAGC | AGGCCATACT | GCGGAAAAAT | CAGAGCAGGT | TTTTGATGTT | ATGGAGAAGT | 120 |
| TTGCAGGTTA | TGGATTTAAT | AGATCTCATG | CCTACGCCCTA | CTCAGCCTTG | GCCTTCCAGT | 180 |
| TGGCTTATTT | CAAAACGCAT | TATCCAGCCA | TTTTTTATCA | GGTCATGTTA | AATTATTCCA | 240 |
| ACAGTGATTA | CTTAATAGAT | GCACTTGAAG | CAGGTTTTGA | AGTAGCCTCT | CTATCCATCA | 300 |
| ATACTATTCC | CTATCACGAT | AAAATTGCCA | ACAAGTCTAT | CTATATAGGT | TTGAAATCGA | 360 |
| TTAAGGGGCT | CCAGCAAGGA | CTTGGCGCTT | TGGATTATTG | AACATAGACC | TTATTCTAAC | 420 |
| ATTGAAGATT | TTATAGCTAA | ATTACCTGAG | AATTATCTGA | AACTTCCTCC | TGCTAGAACC | 480 |
| TTTGGTAAAA | GTTGGTCTTT | TCGATTCATT | TGAAAAAAAT | CGTCCAAAAG | TATTTAATAA | 540 |
| CTTAGCTATC | TATTGAATTG | TGAA | | | | 564 |

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| ACTAATCACT | TACTACGTAG | CTTCTGACTA | TCTACCTCTA | CTAGATAAAG | GACAAACTGT | 60 |
| AAGATTAAAA | CTGGAGAAGN | TTGGAAATCA | CGGCATTACC | ACCATCGGCC | AACTTCAGAC | 120 |
| AATTGATCAA | ACTCCTACCA | GAACAGAGCA | AGGCAATCTC | TTTAAATTAA | CCGCTCTTGC | 180 |
| AAAACATATCT | AATGAGGATA | GTAAACTCAT | CCAATATGGC | TTACAAGGTC | GCGTCACTAG | 240 |
| TGTAAC TGCA | AAGAAAACAT | ATTTTGATTA | TTTCAAAGAT | AAAATTTTAA | CCCATTCTGA | 300 |
| TTAATTTTCA | GATAACACTC | TATAACTATT | TATTATCTTA | TCAAAAAGGA | GAATCATAAC | 360 |
| ATGGATAAGA | AACAAAACCT | AACTTCATTT | CAAGAACTAA | CAACTACCGA | ACTCAACCAA | 420 |
| ATTACAGGTG | GAGAATGGTG | GGAAGAACTC | TTACATGAAA | CAATTTTAA | TAAATTTAAA | 480 |
| ATCACAAAAG | CACTTGAAC | ACCTATTCAG | CTATAAAAAC | AAGACCGAGA | AACAAGAACT | 540 |
| CTCGGTCTTG | TTTTTTATCA | TTCTGCATGT | ATCACAGTAA | GTACCTGACG | AAAGACTTGA | 600 |
| TTTTGGCGAG | GTAGTATT | | | | | 618 |

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| CAGGGGATGC | CAGTTGATTT | GCTTCAAGTT | GACTTGACTC | GTACTTGGGA | AATCCTCGGA | 60 |
| GAAATCACTG | GGGATGCTGC | TCCAGATGAA | CTCATCACCC | AACTCTTTAG | CCAATTCTGT | 120 |
| TTAGGAAAAT | AAGAAAAATC | CATGATCCTT | CATTCGGTCA | TGGATTTTAT | TGTCCTTTATT | 180 |
| AGTAATCTGG | TCTTAAGACC | CCTGTTACAG | TTGCCCTTAGT | TGCTTCGTAG | TCGCCATCTA | 240 |
| CGACAACCTT | GATAATGCGT | TTGACATCTT | CTTCTGGTGC | TGGAACAAGA | GGTAGACGAG | 300 |
| TGGGTCCAGC | TTCAAATCCC | ATATAGTTAA | GAATTGCCTT | AACTGGAGCA | GGACTTGGAT | 360 |
| AAGAGAAGAG | AGCATTAACC | TTAGGAATGA | ATTTACGCTG | AATTGCTGCG | GCTTTCTTCA | 420 |
| TATCGCTTTC | TGCAATGGCA | GTAAACATCT | CGTGCAATTTC | ATCCCCATTT | GTATGAGAAG | 480 |
| CAACAGAAAT | AACCCATCCG | CCCCAAGGTT | CATGGCATGG | AAAGCATCTC | CATCCTCACC | 540 |
| TGTATAAAT | | | | | | 549 |

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
CTGGCTANCA AAATCATACT CATAATCCTT AACACCGACA GAGATAGAAG CAATGAGCCC      60
TTGATCGTGC ATTCGTTTAA TAAAAGGAAT GCGTCCTGCC TCATCAAAAC GGTGCATAAG      120
TGTACAAGTA ACCACCTTTA GCCAGTTGCT CTGCTACATT TTCATCCAAA ATCGTCTGCA      180
TATTCGCTGG CACAACAGGT AGTTTAAAGG TGTGATTTC TAAAGTGACA CTGTATCCG      240
CTTCTGCACG GCTTTTAATG ACACATTTAT TTGGAATCAA TTGAATATCT TCGTAATCAA      300
AAATTGAAA TTCATTTAAC ATATCGATGT CTCGTTTCTT TTGTAATGAC CTACCTATGC      360
TCTCGCATCA CTACGCCTTT TCCGACGTTT CCCTTAAATT TATTATAAAC CAAAAGTACA      420
GTTTTGTCA AATTATTTCA TGAATNAAAT ATATC                                     455
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
CTCCTGGGTT TTGATTAACT CTAGGGTTGC CAAAAGAGG GTGATGACTT CTTGGACATT      60
CTGGGCTTCC TTGAACAAAT CCTGCAAGCG CAATTGATTT CGTCCAATCA AGGATTCTTT      120
CACAATAATC ATCATGTCC CTATCTTATA CTCATCCCGC AAGATAGTCG TGTGATTTTG      180
TGCAAACTCC TCTTTTTTCT TGGCTAGGAT ATTTGAAAAA GCCAAAAAGA GGTCAATGGT      240
CGTCTTGTC TGCACAAGCT CCGCATCTTC GTAAATCAAC TCTATCGGCG CTTTGGGAATA      300
ATACTGGGCC CGTTTCTTGG TGCTTGCTT CCAAGTGCTC ACCCAAGAGC TTGAACCTGC      360
GATATTCTTC GATTGAGAG AGGAGGTCCT GCTCCAGGTC ATCCCCAAG TCTGTCACTT      420
CTGCTACCTT CGGAAGGAGT TTACGACTCT TAATCAGCAT GAGCTGACTA GCCATGACCA      480
TGTACTCACC CGTCACTTCC AGACGATGG CCTGCAGGGT TGAGACATAG GCTAGATACT      540
GTTGATGAC TTCCGTAATG GGCACATCGT AGATATCCAT CTGGTACTTA GAAACCAGAT      600
GCAAGAGTAA GTCCAGGGGT CCTTCAAAAT CTTTAAATTT AATATCCATT ATCTATATTT      660
TTCTAAGGTC AGGACTGTTT TTAATCCTAA TTTTCTTGCA ATTCGTACA AATCGACCTT      720
GTTTTCTATT TGTCTTAGA ATAACTGTT CACGTAAGAC TTGAGATCGA ATTCCT          776
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```

ATTGATACCN ATTGTACAGG ACAACTTATT TTGGAGCGCC ATAGCAGGGA TANGGTTAGC      60
AATAGATGCG NTGACCATAG AAACGTTTNT TAGCCAATAC ATAACCTGCT AGAGATGAGG      120
TTGCACAAAC TAAGAACATG GTTACCAATG AGATAAATAC TGAGTTCCAC ATCCATTGCA      180
AGGCAGGGTT CTGCACCATG AGTTGTTGGA AGTTTTCCAT GGTTGGCATT TTAGGGAACC      240
ACTGAGGAGG AATAACAATT GTATCAGGTT GTGATTTGAA TGCCCCCTGTC AAAATCCAGT      300
AGAATGGAAA GATGNACAGC ACAGTCAACA AGAGCAAAAT GATTGTTGAA ATNACAGTAA      360
AGGCTGTAA TGGTTTTTTT TCTGTAGATT GCATAGCTGT CTCCTTTCTT TAGTATTCTA      420
CGTCGTTTCC AAGTACTTTA AATTGAACAA AGCTTACGAT AGCAATCATG ACTGCCAAGA      480
AGACACCAAT TGTGTTGGCA TAGCCGTATT CTGTCAATTG GAAGGCTTTT TCGTAAAGGT      540
AGTACATCAA GGTACTTGTT GAGTAGTTTG GACCACCAGA TGTCAAAAGC TGAATCAAGG      600
CGAAACACTG GAATGAGTTA ATTGTTGTGA TGATTGCAAT ATAAAGAGTT GTTGAAGAA      660
GGCTTGGCCA TTTAATCTTC CAAAAAAGTT GAACTCAGT TGCACCATCA ACACG          715

```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

CTGGGCTGAG TTTTCCAGAT ACAAATACTG CAACCGCAAC TGCAATCCCC CAACCCATAG      60
TAATCACAAT CCAACCTGCA CTGTTGCTCT TGGTTTTTGG AAGAACCACA CCTGCAACAA      120
CACCATTTC TAGAAGAATC AGGATTAAAG TCCCTAAAAA TTCTCCAAAT AATTCACTCA      180
TCATTTTTCT GTCTCCATTA AAGAAGGG GCGGGCGACA AGGATTGCTA CCCTCCACCT      240
CTTTTATTTT TTCTTAATTT TTTAATTCTG CTAAGTCGTT TTGAGCAAGA GCTGCTTTTA      300
CATCAGCAGC GTAAGTTGCT TTTTCTTCTT CTGTCCAGTC ATAGAATCGT CCCATTTCAT      360
CCAAAAGTGG CTCAACGATA CTATCCAAGC TATCACGCAT AAAGAGCATG TGATTGGTAC      420
GACGAAGAAG GAAGTCAACT GGGCTAAGAG TCAACTCATT GCGCATTGCA TAGTGAAGGG      480

```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

CTTAATTATA ACTTAAACAC AAAAGTTTTC CACAAACTGT GGATAACTCT TTTGAAACTG      60
TGATTTTCTT AATTGAAATC TATTTTATAT TTTGTGAATA AGATGTGAAA AAATAGAGAA      120
TATGTTAGAA TAGAGTCATG AAAATTAAAG TTGTAACAGT TGGGAAACTG AAAGAAAAGT      180
ATTTAAAAGA TGGTATCGCA GAGTATTCAA AACGAATTTC TAGATTGCTT AAGTTTGAAA      240
TGATTGAGTT ATCAGATGAA AAAACACCAG ATAAGGCCAG TGAATCAGAA AATCAAAAGA      300
TTTTAGAAAT AGAAGGTCAG AGAATTTTAT CAAAAATTGC TGACCGTGAT TTCGTTATTG      360
TGTTAGCCAT TGAAGGGAAA ACTTCTTCTC CAGAAGAATT TAGTAAGCAG TTAGAAGAAA      420
CTTCTATAAA AGGANTTCTT ACTCTTACTT TTATTATTGG GGGAAAGTTT GGATTGTCAT      480
CATCTGTAAG AAATAGAGCC AATCTTCTCT TCAGTTTGGG TCGCCTAACC TTGCCTCATC      540
AGTTAATGAG ACTAGTTCTT GTTGAACAAA TCTATCGCGC TTTTACGATT CAGCAGGGAT      600
TCCCTTACCA TAAATAGAGA ATTGACTTTT AATTGAATTT TTGGTAGAAT AATTGTGTGA      660
GGTCTCATAG                                     670

```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

CTATAATTTT ATTAGCTGTA TTCCAGTCGT CACGACCAAA CTCTGTTACA GGGACACGAA      60
TGTCAAAACG GTTCTCAATC TCCACAATCA ACTCAACCGT TCCCATACTA TCCAAGACAC      120
CTGCATCAAA AAGATCTTCA TCCATCATGT CAGAAACATC TTCCATAAAC AACTCATCAA      180
TAATTTTCGAT AACTTCTGAT TTGATATCCA TATTTTATTT CCTTTTATTT TTAAACCAT      240
AGATTATTCA AGAATCCAGA AAAGATTAAG AATGACAACA TGACAACATG GAAAGTGACA      300

```

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACCATGCCAA | GCAACTGAAT | CCAGCGATT | TCAGGTAGGG | CAGCCTTCCC | TGCTTTTTC | 360 |
| CGTTCCTTAT | TGAGCGTTTT | TTTCTTGCGA | ACCCAGGCAT | CATTGATGAA | CAAGCCTAAG | 420 |
| TCCATGAAAG | AGTCCCATAG | GCGATATAGT | ACCAGGTCAC | ACCATGCCAA | AATCCCCATA | 480 |
| ATCCAGCATA | TTTACAATGT | AAGATC | | | | 506 |

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ATGGTTCGAC | CCACAAATAT | GTTTTCGAA | TCATTGACCA | TTCTATGATT | TACGTTGCCA | 60 |
| TTGCCGGCTC | ATACACGCCC | GTTGTCTTGA | CCTTGATGAA | TAAGTGGTTT | GGCTATCTGA | 120 |
| TTATTGTCAT | CCAATGGGGA | ACGACCATCT | TTGGTATTCT | CTATAAAATC | TTTGCTAAAA | 180 |
| AGGTCAATGA | GAAATTTAGC | CTTGCTCTTT | ACCTGATTAT | GGGCTGGTTG | GTTCTGGCTA | 240 |
| TCATTCCCTG | CATTATCAGT | CAAACNACAC | CCGTTTTCTG | GATTCTCATG | GTAAGTGGCG | 300 |
| GACTCTGTTA | TACAGTTGGA | GCTGATTGAT | AGCCTTTATG | CATTGAAATT | TGACAGTTTG | 360 |
| ACTTATGAAA | ATAAAGCAGA | GGTTATGGAC | TTTATCAAGG | CTCGTGTTGA | TAAGATGATG | 420 |
| GGCTCTACTC | CAAAAGATAT | CAAGGGAAGC | AGTTCTTGCA | GGTTCAAAC | TTGTTGTGGC | 480 |
| AGATATGTTT | GGAAGCAGCA | AGTGCTCTCG | TAGAAGTAAG | CAAGGAAGAA | GATTTTAAAC | 540 |
| CATCTGTTGA | ATCACTTTCT | CGTGCCCTTA | ACCTGGCTGA | GAAGGCAGAA | GGGGTTGCTA | 600 |
| CAGTTGATT | AGCACTATTT | GAGAATGACC | AAGAAAAAGC | TTTGGCAGAA | GCAGTAGAAA | 660 |
| CACTCGTTTT | ATCAGGACCT | GCAAGTCAGC | AATTGAAACA | ACTCTTTGCG | CTTAGCCCAG | 720 |
| TCATTGATGC | TTTCTTTGAA | AATACTATGG | TAATGGCTGA | AGATCAGGCT | GTCCGTCAAA | 780 |
| ATCGTTTGGC | AATCTTGTC | CAACTAACCA | AGAAAGCAGC | TAAGTTTGCT | TGTTTAAACC | 840 |
| AAATTAACAC | TAAATAAAAT | TTGATAAAG | GACTTTATCT | TATTACAAAG | GAGAAGAAAT | 900 |
| GGATCCGAAN | ANATTGCTCG | T | | | | 921 |

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

| | |
|--|-----|
| CTTGGCAACA GGCTCTTTTT GTATTGCGTT TATTAAGAAA AACAAAAAAC ATCGATATAA | 60 |
| CATTTAACTA AAAATTATTG TATGTTATCT CCCTTAATTA GGAATGATAA GGAATAACT | 120 |
| AGAAAGATTT GTGAATACAA ACTATTTCTG ATATACAAAA TATACAGTAA TAATGAATGA | 180 |
| TGGGAGATGG GATGAAAGAA TTTCAATTG AGAGAAAGCA GCGTTTTTCT TTGAGGCCAT | 240 |
| ATGCAATAGG AGCTTGTTCTG GTCTTGCTAG GAACGAGTTT ATTTTTTGCT GGTATGGGTG | 300 |
| CTCAGCCTGT ACAGGATACA GAAACGAGTT CAGCACTAAT TTCAAGTCAT TATTTGGATG | 360 |
| AGCAGGATTT ATCTGAAAAG CTGAAATCTG AGTTGCAATG GTTTGAATTA GAAAACAAGC | 420 |
| TTTTGAACTT ATGGGAACAT TAGGTTACTA TGAAGGATTT GTTCCTTATG TTTCAAATCA | 480 |
| ATACAAAAAC CAAGCTGAAG AAGAAGGCAA ACCGCTATCT GATAAATATA TTTTCGAAAA | 540 |
| ATCTTAAGAA AAACATATGC ACCTTCAAAA A | 571 |

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

| | |
|---|-----|
| GTATCAACTC CAAAGAGCAA GTGACTGTCA AAGTTGTAAC AGATGCGGCC AAGAAGCTCA | 60 |
| TGGGTGATAA GATTGCTCGC CAGAAAGAAC GTGGGATTCA GATTGANACC TTGCGNACCA | 120 |
| TGATTATNGG GATTCCANAC GNTGGTAAAT CCACTCTGAT GAACCGTTTG GCTGGTAAAA | 180 |
| AGATTGCTGT TGTTGGAAC AAGCCAGGGG TCACAAAAGG TCAACAATGG CTTAAACCA | 240 |
| ATAAAGATCT GGAAATACTT GGATACACCG GGGATTCTCT GGCCTATAGT TTGAGGATGA | 300 |
| AACTGTTGCA CTTAAGTTGG CATTGACTGG AGCTATCAAG GATCAGTTGC TTCTATGGA | 360 |
| TGAGGTTACC ATTTTGGTA TCAATTATTT CAAAGAACAT TATCCAGAAA AGCTGGCTGA | 420 |
| ACGCTTCAA CAAATGAAAA TTGAAGAAGA AGCGCCTGTG ATTATTATGG ATATGACCCG | 480 |
| CGCCCTCGGT TTCCGTGATG ACTATGACCG TTTTACAGT CTCTTCCGTG AAGGAAGTCC | 540 |
| GTGATGGCAG ACTCGGTAAC TATACCTTAG ATACATTGGA AGACCTCGAT GGCNACGATT | 600 |
| GAACTAAGTC C | 611 |

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1054 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

TTGCTAAAGC AGCCATGATG ANGGCACTCC ATAAGGATAA GTACCACCAA GCAGCAGCAG      60
ANGACCATAA TCTCCTTTAT GACTTGAACG AGAACGTTCA ATAATAACTT TTTCTAGTAA      120
GGTTTGATTA ATCACTTTCA TCCTTTTTCG CTCTCACTTT TATTATACAA CAAAAAGGAG      180
ACGCAGACCT CCTTTTGTA TCTTATATCT AAAATTTAAT ATTCATTCTT GCCATTTTAG      240
ATATAGCTAT AGAAAATACA CTCTATTAAT CGAATGTTTC TCTTATTTTC TATCCAATGT      300
CCGAAGTGCT GCTTGATAAG TTTGCTCCAT CAGCATGGTA ATGGTCATAG GACCGACACC      360
TCCAGGGACT GCGTGATAT GGCTAGCAAG TGGTGCAACT GCCTCATAAT CAACATCTCC      420
ACAGAGCTTC CCATTTTCAT CTCGGTTCAT CCCAACGTCA ATGACAACCG CACCTGGTTT      480
GACAAAGTCA GCAGTCACAA ACTTGCGCGG GCCGATTGCG ACTACAAGAA TATCTGCTTT      540
AGCAGCCACC TTGGCAAGAT TATGAGTTCG TGAGTGGGCC AAGGTTACTG TCGCATTTTT      600
AGCCAAAAGA AGCTGAGCCA TAGGTTTTCC AACGATATTT GAACGACCGA TTACGACCGC      660
ATTTTTACCT TCCAAGTCAA TCCCATATTC ATGAAACATT TCCATAATTC CTGCAGGTGT      720
CGAGGGAATC ATGACTGGAT GTCCAGACCA AAGACGTCCC ATGTTTAGGG GATGGAAACC      780
ATCCACATCC TTTTCTGGGT CAATGGCTAA TAAAACCGCC TCTTCATCGA TATGTTTTGG      840
TAATGGCAAC TGGACCAAAA TCCCATGCCA AGCTGGATCC CTGATTATAT TTAGCAATCA      900
GGTCTAACAA TTCCTCTGA GTTAATGGTC TCTGGAATC GCACTACTTC GCTACGGGAA      960
CCAGCCGCAA GAGCTGACCT CTCCTTGTG CGAACGTTAA ACTTGGCTGG CTGGATTATC     1020
CCCAACCAAA ATCACTACCA ACCAGGCACT AGAG                                1054

```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```

CTGAACTGGA TTTTGCTACA AGGTCTGATT TGTCAAAGAG ATGCGAGTTA TGATATGAAG      60
CAGGATGATT TGGATAAGGT AGCAGATTAT CTCTTCAAAA CAGAAGAATG GACCATGTAT      120
GAGTTGATTC TTTTCGGTAA CCTCTATAGT TTCTACGATG TAGACTATGT CACTCGGATT      180
GGTAGAGAAG TTATGGAGAG GGAGGAATTT TACCAAGAGA TTAGTCGCCA TAAGAGATTA      240
GTGTTGATTT TGGCCCTCAA TTGTTACCAG CATTGTTTAG AGCATTCCTC TTTTATAAT      300
GCCAACTATT TGGAGGCTTA TACAGAGAGG ATTATTGACA AAGGTATTAA GCTTTATGAG      360
CGTAATGTTT TCCATTATTT AAAAGGTTT GCCTTATATC AAAAAGGACA GTGTAAGAA      420
GGCTGTAAGC AGATGCAAGA GACCATGCAT ATTTTGTATG TGTAGGTCT TCCAGAGCAA      480

```

| | |
|---|-----|
| GTTAGCCTAT TATCAGGAAC ACTACGAAAA ATTTGTCAAA AGTTAATTTT CCCAAATAAG | 540 |
| GGAAAAAATA AAAAGCTCCT TTCGGTTTGT ATACAATAGT TTCAAAATTT GAGAGGAG | 598 |

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

| | |
|---|-----|
| CTACTTCCCG GCCGAGTCGA TTCTCCGCCG ATATCGAGCA TACTGGCTCC TTCTGTTATC | 60 |
| AATTTACGAG CCTGCTGGAG CGCTGCTCA AGAGCAAAAA ATTGACCACC GTCCGAAAAG | 120 |
| GAGTCTGGGG TTACATTGAT AATTCGCAA ATAGCTGTCT TTGCATGAGT GGCTTTACTG | 180 |
| GACATATCGG TCACTCCCTC AAGGCTATTC ATCATATTAT TTCTCTATTT TACCATAAAA | 240 |
| AGAAAAAGAT GGACACGATT TCATTCATCT TTCTCCCACT AGAAACAAGT AAGCAATTGT | 300 |
| CAATAATCTT AAACAGAAAT CCCTAATGTC CGACTCATAA TCACCACAAG AGCCAACAAA | 360 |
| CAGAAAGCAA TCCCATTAAC AATCATGTGA AGTAAGATCG ACATTTCCAA ACGTTGGGTC | 420 |
| TTGTAGGCTG TCCAAGATAG AACTGTCGAC ATACCTCCAT AAATCAATAA AGAAGGTAAA | 480 |
| TTACTTGGTT GATGTAATAA AGCAAACACA ATCGTACCGA CTACAAAT | 528 |

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

| | |
|---|-----|
| CTATGAGAGA GAATGACCTT CTCTTGATTA CTGCGGACCA TGGAAATGAC CCAACGTATG | 60 |
| CAGGAACGGA TCACACTCGG GAATATATTC CATTGTTGGC CTATAGCCCT GCCTTTAAAG | 120 |
| GAAATGGTCT CATTCCAGTA GGACATTTTG CAGATATTTT AGCGACTGTT GCCGATAACT | 180 |
| TTGGTGTGGA AACTGCTATG ATTGGGGAAA GTTCTTTAGA TAAATTGGTA TAAGATGACG | 240 |
| CGCTATGCTT TGCTGGTGAG AGGTATCAAT GTTGGTGGTA AGAATAAGGT CGTCATGGCG | 300 |
| GAGCTTCGTC AAGAATTGAC AAACCTGGGA CTGGAAAAAG GTTGAGAGCT ACATCAATAG | 360 |
| TGGCAATATT TTCCTTTACT TCGATAGATT CCAAAGCCCC AATTGGTTGA AAAAGCTAGA | 420 |

GACTTTCTTT GCAGTCCATT ATCCATTTAT TCCAGAACTT TTTCCTTTAC TGAGTCTAGA 480
GGACTTTGAA GGGCGGAACT TGAAA 505

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CTATTTCTC ATCTTTTTTA GACTGGTAAT GTATCCCCTA GAGTTTCATT GTTAAGACCT 60
GTCGTATTGA CAACAGTGGG TCCTGATTCC CCATTCCAAG AGTTTGGCCC GCATCATATN 120
GACGAAATCT TTTCTGAGC CAGCAATTTT CTCAGCTAGG GCAATAGCGG CGCTGTTGGC 180
ACTAGATACC AGAGTTGCTT CAAGCAACTC TTCGACAGTA TAATTACGGG CCTCCATAGG 240
AATATTACTG GCTTCAGAAT TTGTCGTCAA TTGATAAGGA TAATCAGAAA TATCTACAGG 300
AGTGGAGAGG GTAATACTTC CGTTTTCCAA AGCTTCATAG ACCAGATAAA CAGTAATCAA 360
TTTTGTTATG GAAGCAATTT CGACAGGTGG CGTTGCATCC TTCTCATAGA GAATTTTACC 420
AGTATTTGCC TCAACAGCAA TCGCATGTTT AGCGGCAATG GTAAATCTT GAGCAACAGC 480
AGTAGAAGCA CCCCCTAAAA GAGAGACAGT TAACAAAGTT AAAAATATTT TTTTCATAGT 540
AGTCTTATTC TATCATAAAG AAAAAAATA TTCTTGCTTT AATAATTCAT CTGTAAAGCT 600
TTTTGAAAAT ATGGTAAAAT AAAGTGAGGG AGGTAACCTA TGTTTCGTAG AAATAAATTA 660
TTTTTTTGGG CCACAGAAAT TTTACTCTTA ACCATCATCT TTTACCTATG GAGACAGATG 720
GGGTCTTTGA TTAACCCCTT TGTAGCGTG CTTAATACAA TTATGATTCC ATTTTATTA 780
GGGGGCTTTC TTTATTATTT GACAAACCTT ATTGTTACTT TCTTAAATAA AGTCTGTAAA 840
CTCAATCGTT TGCTTGGTAT TTTAATTACC TTGTGT 876

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CTTGTCAAAT GCCATGGAAG GGGTTCTTTA CTTCTCAAA CCAGACTTTT CAAAAGTGAC 60

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TAGCGCTGAT | CTCCTCTATG | CTCTGGGACA | ATCTTTCTTT | GCCCTCTCAC | TAGGGGTAC | 120 |
| AGACATGTTG | ACCTATGCTT | CTTACTTGGA | CAAGAAAACC | AATCTAGTCC | AGTCAGGAAT | 180 |
| CTCCATCGTA | ACCATGAATA | TCTCGATAGT | CCATCATGGA | AGGTCTAGCC | ATTTTCCCAG | 240 |
| CCATGTCAGC | CTTCAATATC | CACTCTGAAA | GGGGACCCAG | CCTGCTCTTT | ATCGTCTTGC | 300 |
| CTCAACTCTT | TGACAAGATG | CCTTTTGGA | CCATTTGCTA | CGTCCTCTTC | CTCTTTGCAA | 360 |
| CTGTCACTTC | TTCTGTCCGT | GATGCTGGAG | ATCAATGTGG | GCAATGTCAC | CAACCAGGAT | 420 |
| AACAGCAAAC | GTGCCAAATG | GAGTGTATT | TTAGGAATTT | TGACCTTTGT | CTTTGGCATT | 480 |
| CCTTCAGCCC | TATCTTACGG | TGTCATGGCG | GATGTTTACA | T | | 521 |

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGCAGACAA | TAAGTTGGTT | AGCTTAACGG | CTCTTGAGGA | TTCATCCAAG | GATGTAACCT | 60 |
| TTACCAGTTC | GGCTTTCAAT | CTAAAAGAAG | GGCGACACCT | TCAAAAAGGG | GATTCCAAGA | 120 |
| AAATCCTTAT | CCACGAAGAA | TTGGCTAAGA | AGAACGGTCT | TTCATTTCAT | GACAAGATTG | 180 |
| GCTTGGATGC | TGGTCAGTCT | GAATCTGGAA | AAGGACAAAC | AGTAGAGTTT | GAGATTATCG | 240 |
| GCATCTTTCC | TGGTAAAAAA | CAAGAGAAAT | TCACAGGCTT | GTCTTCTGAC | TTCAGTGAAA | 300 |
| ATCAAGTCTT | TACAGATTAT | GAAAGTAGCC | AAACCCTTTT | GGGCAATAGT | GAAGCTCAAG | 360 |
| TCAGTGCAGC | ACGCTTCTAT | GTTAGAAAAT | CCTAAGGAAA | TGGACGGACT | CATGAAGCAG | 420 |
| GTAGAAAAC | TGGCCTTGGA | AAATCAAGGC | TACCAAGTCG | AAAAGGAAAA | CAAGGCTTTT | 480 |
| GAACAAATCA | AAGACTCAGT | TGCAACTTTC | CAAACCTTCC | TGACCATCTT | CCTTTATGGA | 540 |
| TGTTGATAGC | AGA | | | | | 553 |

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

| | |
|---|-----|
| CTATGGATGC GGAAGTTTCT AAGAACCTTC GCTTGATCCT TGAGCGTAAA GGAATGACCA | 60 |
| TCTTGACTGG TACTAACTG CAAGAAATCA TTGAGGAAAA TGGTCAACTT CGTATCAAGG | 120 |
| TTGAAGGAAA AGACAATATC ATCGCAAGCA AAGCTCTTCT TTCAATTGGT CGTATGCCAG | 180 |
| ACCTTGAAGG TATTGGAGAG GTTGAGTTTG AATTGGATCG TGGTTGTATC AAGGTCAATG | 240 |
| AATACATGGA AACTTCAGTT CCACGCATTT ATGCCACCAG GTGACATCAA CGGTACTAAG | 300 |
| ATGTTGGCTC ACGCAGCTTT CCGCATGGGT GAAGTTTCCG CTGAAAATGC CCTTAAAGGA | 360 |
| AATCATGCAG TTGCCAAATT GAATTGACT CCTGCAGCCA TCTACACTCT CCCTGAAGTA | 420 |
| GCAGCAGTAG GTTTGACAGA AGAACAAGCC CGTGAGAAAT ACGATGTTGC CATCGGTAAG | 480 |
| TTTAACTTTG CTGCTAACGG TCGTGCTATT GCATCTGACG CAG | 523 |

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

| | |
|---|-----|
| CTGCAGGTGG AATTATGAAT GTCGGATATG AAAAAGCATT CTTGATGCAG ACATCGTTAA | 60 |
| ATTTGCCAAC TTCTGAAATT ATCTCGACAT ATGTCATAAA AGTTGGTCTT GTATCAGGAG | 120 |
| ACTATTCTTA CTCAACAGCG GTTGGTTTGT TTAATGCAGT GATTAACGTA GTATTGCTTG | 180 |
| TTGCAGTTAA CCAAATCGTT AAACGCATGA ATAATGGTGA AGGAATTTAA GGAGGAAAGT | 240 |
| ATGAAAAATT CGATTATGGA TACAAAATTT GATAGACGTA TCTTACTCTT AAATAAAATC | 300 |
| ATTATTGTCT TTATCGTTTT GATGACTTTG CTTCCTTTAC TTTATATCGT CGTAGCATCC | 360 |
| TTTATGGATC CTAAGGTTCT GGTTAGTAGA GGGATTAGCT TTAATCCAGC CGATTGGACT | 420 |
| GTAGAAGGTT ACCAGCGTGT TATTCAGTGA CCAATCTATT CTAAGAAGTT TTATCAATTC | 480 |
| CCTACTATAC TCTTTTGGAT TTGCAGCT | 508 |

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| CTAAAAAGAA | CCAGATGGAT | CTTGTGATGA | ATTTACATCA | TTTTGATTTA | CCAGTGGAAC | 60 |
| TTCTTCAAAA | ATACGGTGGT | TGGGAAAGCA | AACATGTAGT | GGAGTTATTC | GTGAAGTTTG | 120 |
| CCAAGACTGC | TTTCAACATG | CTTTGGAGAT | AAGGTTTCATT | ACTGGACAAC | TTTCAATGAG | 180 |
| CCAATGGTCA | TTCCAGAAGC | AGGATACTTA | TATGCTTTCC | ATTATCCAAA | TCTAAAAGGA | 240 |
| AAGGGAAAAG | AGGCCGTACA | AGTCATCTAT | AATCTAAACC | TTGCTAGTGC | AAAAGTGATT | 300 |
| CAACTATATC | GCTCATTAGG | ACTTGATGGA | AAGATTGGGA | TTATTTTAAA | CTTGACACCT | 360 |
| GCTTATCCAA | GAAGTAATTC | TCCAGAAGAC | TTAGAAGCAA | GTCGATTTAC | AGATGACTTC | 420 |
| TTTAACAAAG | TCTTCCTTGA | ATCCAGCTGT | TAAAGGAACT | TCCCAGAAA | AGATTGGTAA | 480 |
| AAACAGCTAG | AGAGAGATGG | CGTGTATGG | AGTCATACCG | AAAAAGAG | | 528 |

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTCTTATTG | GTGAGGTATC | GCAACTTCTG | TTTCTGCCTT | CCTTGGTGGA | CCAGCCAATA | 60 |
| CAACTTACGG | AGAAAATACA | GGGGTTATCG | GTATGACTCG | TATCGCTTCT | GTCTCAGTTA | 120 |
| TCCGTAACGC | TGCCTTCATC | GCGATTGCCC | TCAGCTTCCT | TGGTAAATTC | ACTGCCTTGA | 180 |
| TTTCAACTAT | TCCAAACGCT | GTACTTGGTG | GTATGTCAAT | CCTTCTCTAT | GGGGTTATCG | 240 |
| CCAGCAATGG | TTTGAAAGTC | TTGATTAAAG | AACGTGTGGA | TTTCGCTCAA | ATGCGAAACC | 300 |
| TCATCATCGC | AAGTGCTATG | TTGGTTCTTG | GACTTGGGAG | GAGCTATCCT | TAAACTTGGT | 360 |
| CCAGTTACAC | TTTCAGGTAC | TGCCCTTTCA | GCCATGACAG | GAATCATCTT | GAAGTTGATC | 420 |
| TTGCCATACG | AAAATAAAGA | CTAAGAGTCT | AAATACACCT | AATCCACTCA | GACAGCTGAG | 480 |
| TGGATTTTTC | GTATACCATA | ATAAAAGTGT | CTTAACAAAA | TTATTAAAAT | CAAAAAACGT | 540 |
| ATAATATCAG | ATATTCTAAA | ACCTTGATAC | TGTACGTTTT | ATCATAGAAA | TTTTTACTTT | 600 |
| ATTTTCTCAT | CAAATGAGAT | TGTCATCAAT | CTCTTGTCTT | ACTTGCCTTT | CTTCTTCGCT | 660 |
| TTCTTCATTT | TGTTAGCCAT | ACGTTTCATG | GACTGTTTCA | TGGCAAATTC | ACCAATTTTA | 720 |
| CCTTTCAAAC | CGCCACCAAA | CATCTGGCTC | ATATCTGGCA | TTCTGCTCC | TCCGAGAG | 778 |

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```

GGGAGTTGGT TGCTATTNGT GAGGGAAAAG GTTTGAACTT TGAAATCGAA GTGGATGGTG      60
GGATTGATGA CCAAACCTATT GCTCAAGCCA AAGAAGCTGG TCGGACTGTT TTTGTAGCAG      120
GTTCCATATG CTTTAAGGGA GAAGTCAATG AGCGAGTACA AACTCTCAGA AAACAACCTGG      180
ACTAGGGTTG CAGTTTTTGC AGGCGGAAAC CGCGGTCATT ATCGGACAGA TTTTGATGCT      240
TTTGTGGGG TGGATCGAGG CTCGCTCTGG GTCTTGGAAG AAGACTTACC TCTTGCTCTA      300
GCAGTCGGAG ATTTTGATTG TGTGACGGAA GAAGAGCGAC AGGTGATTCA AAAACGTGCC      360
CAGTATTTTG TCCAAGCCCC GCCAGAAAAA GATGATACTG ATTTGGAATT GGCTCTCTTA      420
ACCATCTTTG AACAAAATCC TCAGGCTGAG GTCACTATTT TCGGTGCCTT GGGTGGCCGT      480
ATTGACCATA TGTTGGCCAA TGTCTTTCT ACCTAGCAAT CCCTAAGTTG GCACCCTATA      540
TGC GTTCNAA TAGAAATTGA GGAATGGGCA AATTTGATTG CCTATTGTTC CAGAAGGGAA      600
CAGTCAGATT CGAATCCCTG CA                                         622

```

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

CTATTATCAG CACTTTTATA CCTATTACCA AAAAAATCCT CAAAATGATT GGCAAAAGGC      60
TTTATCCACC AGCCATTTAT CAGCAATATT TACTTGAAAA ATATGGTAGA AATAGAAAGG      120
ATGGAGGAAT CTAATGGTAT TACAAAGAAA TGAAATAAAT GAAAAAGATA CATGGGATCT      180
ATCAACGATC TACCCAACCTG ACCAGGCTTG GGAAGAAGCC TAAAAGATT TAACAGAACA      240
ATTGGAGACA GTAGCCCAGT ATGAAGGCCA TCTCTTGGAT AGTGCGGATA ACCTACTAGT      300
AAATCACTGA ATTTTCTCTT GAAATGGAAC GCCAGATGGA GAAGCTTTAC GTTTATGCTC      360
ATATGAAGAA TGACCAGGAT ACACGTGTAA GCTAAGTATC AAGAGTACTA TGCCAAGGCC      420
ATGACACTCC TACAGCCAGT TAGACCAAGC CTTTTCATTC TATGATCCTG AATTTATGGA      480
TATTAGCGAA AAGCAGT                                         497

```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

| | |
|---|-----|
| CTGTTATGGA GTTGAAAGAA GAATACCACC CAGACGGTAA AGGTTTGTAA ATGATCTGTA | 60 |
| TCGGTGGGAT GGGAGCTGAT TTCTTTAAGG CTCGCGGTAT TCAACCACTT TATGAATTAC | 120 |
| GTGGCTTGTC AGACCAACCT AGCTTTGATC AAGTTCGTAA GATTATTTCA AAAACTGTTG | 180 |
| AAATGTACCA AAATGAACTC TTTGATGAGC TTTATGTTTG CTACAACCAC CATGTCAATA | 240 |
| CGCTAACCAG TCNAATGCGT GTGGAACAAA TGCTTCCGAT TGTGACTTG GATCCAAATG | 300 |
| AAGCGGATGA AGANTACAGC TTGACTTTTG AAATTGGGAA ACCAGCCGAG AAGAAATTCT | 360 |
| GGAGCAGTTG TTGCCTCAGT TTGCAGAAAG TATGATTAC GGTGCCATTA TCGATGCCAA | 420 |
| GACAGCTGAG AATGCTGCGG GTATGACAGC CATGCAAACA GCGACAGATA ATGCTAAGAA | 480 |
| AGTCATCAAT GATTGACAA TTCAGTATAA CCGTGCCCAG ACAGGCGGAT ATTACACAAG | 540 |
| AAATTACCGA AATCGTAGCA GTGCCTAATG CCTTAGAATA GCTCTAGTCC CAGCTCTCCT | 600 |
| CACTC | 605 |

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

| | |
|---|-----|
| CTACACTTGA GGAAGTTTG AAAATTCCAT TTTCTTAAA GGAATTGTG AAACGCTATG | 60 |
| TATTTTCTTT TTACAACCGG ATGGAGCACT TGTTGTGGT CAATCCTATG TTTATTGAGG | 120 |
| ATTTGGTAGC AGCTGGTATT CCACGTGAAA AAGTGACCTA TATTCCTAAC TTTGTCAACA | 180 |
| AGGGAAAAAT GGCATCCTCT ACCACAAGAA GAGGTAGTCA GACTGCGCAC AGATCTTGGT | 240 |
| CTTAGTGACA ATCAGTTTAT CGTAGTAGGT GCTGGGCAAG TTCAGAAACG TAAAGGGATT | 300 |
| GATGACTTTA TCCGTCTGGC TGAGGAATTG CCTCAGATTA CCTTTATCTG GGCTGGTGGC | 360 |
| TTCTCTTTTG GTGGTATGAC AGATGGTTAT GAACACTATA AGAAAATTAT GGAAAATCCC | 420 |
| CCTAAAAATT TGATTTTTC AGGCATTGTA TCGCCAGAGC GGATGCGCGA AATTGTATGC | 480 |
| TCTAACGGAT CTTTCTTGT TGCCTAATTA CAATGAG | 517 |

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| TGTTGCGCTC | CATATCCNAA | ACTTGCCCTG | CCACCATAACC | CAGACTACCT | GAAGCAAGGG | 60 |
| ATAAGTTGGC | AATCGAGCCC | ACCTNGATCT | GACTTGGCGA | ATCTGCCTGC | GCAATCAAGG | 120 |
| CATATGGGTC | TAAGAATAAG | GATCTCCAGC | CAAAATGGCC | ATAGCTTCAC | CGAATTTCTN | 180 |
| GTGATTGGTT | AACCGCCCTC | TTCGATAATC | GTCATCATCC | ATAGCAGGAA | GGTCATCGTG | 240 |
| AATCAAGCTC | CCTGTATGAA | TCATCTCCAA | GGCAGTAGCT | ACCTGCGCGN | GAGCAGGTTT | 300 |
| GATGGTAACC | TGCAAGGCTT | CCAGAACTTC | TAACAAGAGA | AAAGGCCGAA | TACGCTTGCC | 360 |
| ACCAGCATGA | ATAGAATAGA | GAACAGACTC | CCGTAAACTA | GAGGCAAACT | GCTGGTCTCC | 420 |
| ATAAAATCTT | CCAAAGCCGA | CTCGACAAGA | GCTAATTTTT | CTTGCTTTTT | CATTCAAAT | 480 |
| CACTTTCTGT | TCCGTCTTCT | TGCATGACCT | TGACCAAGGT | CTTTTCAGCC | TTGTCCAGCG | 540 |
| TAGCTTGGAG | CTCTTTTGAC | AAGACCATGC | CCTTTTGAAA | GGCAGTAATC | GCATCTTCCA | 600 |
| GAGCAATTC | ACCATTTTCC | AAACTTTGGA | CAATGGTTTC | CAGTTCTGCT | AGATTTTCCT | 660 |
| CAAATTTCTT | TTGTTTGGAC | ATCTTTAACC | TCTAATTCTA | CTTGACCATC | TCGCATCAAA | 720 |
| AGCGTTACTT | GGTCTTTTTT | CTTCAAATC | TCAACCGAAT | CTACAACGGA | TCTTCTTTTT | 780 |
| TGACAATAGC | ATAACCAC | | | | | 798 |

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCATGTTTGC | GGCAGTGACA | GCAGGTTATC | AGGCTGCCCT | AATGGTACCA | ACAGAAATCC | 60 |
| TCGCAGAGCA | ACACTTTGAG | AGTTTACAGA | ACCTTTTTC | CAATTTGAAA | CTGGCTCTCT | 120 |
| TGACAGGTTT | CTTGAAAGCT | GCAGAAAAGA | GAGAAGTCTT | GGAGACCATT | GCCAAGGGTG | 180 |
| AGGCTGATTT | GATTATAGGA | ACTCACGCTC | TGATACAAGA | TGGGGTGGAG | TATGCTCGTC | 240 |
| TTGGTTTGAT | TATTATCGAT | GAGCAGCACC | GTTTTGGTGT | AGGGCAAAGG | CGTATTTTAC | 300 |
| GGGAAAAAGG | CGACAATCCA | GATGTCCTCA | TGATGACGGC | GACTCCCAT | CCACGGACGC | 360 |
| TTGCCATCAC | AGCCTTTGGA | GATATGGATG | TTTCCATTAT | CGACCAGATG | CCAGCAGGTC | 420 |
| GGAAGCCCTA | TTGTGACGCG | CTGGATCAAA | CATGAGCAAC | TACCTCAGGT | CTTGACTTGG | 480 |
| TTAGAGGGGG | AAATTCAAAA | AGGTTCCCAA | GTCTATGTCA | TCTCTCCTTT | GATTGAAGAA | 540 |

TCAGAAG

547

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

CTCTTTTAAC CGTTTTAGCG GTGACACCGA GGTATTTTTT CAGGACCCAA GACTTGTCGG      60
GCAACCGAAA CTGGGAGTTC GTCATCTCCA ATATGCAGAC CAGCAGCATC AACCGCAAGA      120
CAAACATCCA ACCGATCATC GATTATCAAG GGGACCTGAT AGGCATCTGT TATTTCCCTG      180
ACTTGTTTTG CCAGTTGATA ATATTGATTG GTTGTGAGAT TTTTCTCTCG CAATTGGACT      240
ATGGTAACCC CTGAACGGCA GGCCGTCTCA ACTTTTGCAA GAAAGCTTTC CACGGAATCT      300
TGATAGCGAT TGGTTACCAG ATATAGTCTA AGCGCTTCTC TATTCATAAA CCTCTCCTTT      360
GATGGTATCT AGCCAATTTT CATCTCTTCT TAGGAGCGAA AGCTGATTGA GTACTTGGTA      420
ACGAAATTCT TCCAATCCCA TTCCTTGAAC AACTATTTTC TCAGCCAGCG ATATTGAGAT      480
AAGAGACTGC TAAGCAAGAA CTTCAAAACC AGTCTTTCCT TGGCTGAGAA AAACAG      536

```

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

CTGGAGTGAC GATTGAGAAA ATCTTTGCCC TAGAAAATTA TCGAAATCAG TTAGCTGCTT      60
TTCCGCAAAC TGTCTGGATT TCAGAGGATA TTTTGCTAGA TTTGGCGGAT TCTCAGACTC      120
CACAGGGAAT TGTTGCCGTG GTTCAAAAAG AAGAAGTAGG ACAAGCTGAT TTGAGTCAGG      180
GCAAGTTCTT GTTTTGGAA GATGTGCAAC ATCCTGGTAA TGTAGGAATC ATCATTCGAA      240
CTGCGGATGC AGCAGGTTTT ACAGGAGTGA TTGTTTCAGA TAAGTCGGCA GACATCTACA      300
GTCTTCAAAA CCTACGTTT CATGCAAGGT AGTCATTTCC ATCTGCCCAT TTACCGGATG      360
ACTAGTCAAG CGCTTCTTGA CGAAACTAAA AAGGTAGCTA TCCCAGTGCT AGCAACAACC      420
CAATCTAAAG ATTCTGTTGA TTACAGAGAA CTGCCTTCTA TAGAAAATTT TGTACTAGTT      480

```

| | |
|---|-----|
| ATGGGAAATG AGGGTCAAGG AATTAGTCCC CTTATGGCTG AAAGTGCAGA CCAGTTGGTC | 540 |
| CATATTAGCA TGAAGGGGCA GGCCGAGAGT TTGAATGTTG CCGTTGCAGC CCGTATTTTA | 600 |
| ATCTTCCATT TAAGCTAATT TTAACTTTTT TTGTTATAAT CAAGGAAAGA TGTTCACAGA | 660 |
| AAAGGAGAAA TGGATGAATC AACTATTAT ACATGACCGT GCAGGTCTCA ATCAATTTTA | 720 |
| CGCTAAGGTT TATGCCTTTG TTGGTCTGGG AATCGGACTA TCTGCTTTGG TATCAGGCCT | 780 |
| TATGTTGACG GTCTTTCAGT CTCAGTTGGT TTACTTTTTG ATGCAGGGGC GTCTCTGGTT | 840 |
| GACCATTGCT ACTT | 854 |

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

| | |
|---|-----|
| CTGAAGAAAT CCTAAAAGAT TTGTATTACG GAGCCGCTAA GAAAATTCAA GAAGAAGCCT | 60 |
| CTCGCTGGGC AGGAGTTGTA AGAAATGACT AAAACAGCCT TTTTATTTGC TGGTCAAGGT | 120 |
| GCCCAGTATC TACGGATGGG ACGGGATTTT TATGATCAGT ATCCGATTGT CAAAGAAACG | 180 |
| ATTGATCGAG CGAGTCAGGT GCTCGGTTAT GATTTACGTT ATCTCATCGA TACGGAAGAA | 240 |
| GACAAACTCA ATCAGACCCG CTATACGCAA CCAGCCATTC TAGCGACTTC GGTGCTATC | 300 |
| TACCGTTTAT TGCAAGAAAA GGGCTATCAC CCTGATATGG TTGCTGGTTT GTCTCTTGGA | 360 |
| GAATACTCTG CCTTGGTGGC AAGCGGCGCC TTGGATTTTG AAGATGCCGT TGCCTTGGA | 420 |
| GCTAAGCGTG GAGCCTATAT GGAAGAAGCG GCTCTGCTG ACTCTGGCAA GATGGTAGCA | 480 |
| GTTCTCCATA CCCCCTAGAG TCCTTGAGAA GCCTGTCCAA AGCTCTGACT TGAGTGGTAC | 540 |
| TCCAGCCACT ATACACACTG CACAATCTCA TTGCTGGAAA ATTGTTGCAG TGATCAACGG | 600 |
| TGACTTTGCA GAGCAGTGCC AACCCATATCC CCTAGT | 636 |

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| CTCTAAAACG | AATTCTCTAC | AAGCACC GCA | AGGGCATGGC | TGAACTTCCA | CCATAAGGTG | 60 |
| GTTTGCTCTG | AAAGGCTAAT | ACTTCNTTAA | CCTTAGTTTG | TCCTGAAAAT | TGGTACATAT | 120 |
| TGAAGAGGGC | CGCCCGTTCT | GCGCAGAGAT | GGAAAACACC | ACAGGTTCCC | TCCATACAGA | 180 |
| ATCCTGTAAA | TATTTGTCCA | TCTCCTGCTT | CTACTGCAGC | TACAACATGA | TTGGCATAAA | 240 |
| CAAAGTCTGA | TACTTCATGT | GGATTGTATA | GTTTCTGTGC | TTCTTCCTAC | ATCTTTTCCC | 300 |
| AGATGTCCAT | TATTGTATCC | TCTATATTTA | GAGATTTCTT | TTAGAATGTT | TTCGATATGC | 360 |
| TGAATTGATT | TTTCACGTCC | AAGCAAGAAA | ATTGTATCTG | GTAATTCTGG | CCCATGCATT | 420 |
| TCGCCTGAAA | CTGCGATACG | AATAGGCATG | AAAAGATTTT | TCCCTTTAAT | ACCTGTTTCT | 480 |
| TTTTGGACTG | CTTTAATTTG | CGGGAAGATA | TTTTCTGTCA | CAAATTCATC | ATCTGTCATC | 540 |
| CGCTTCAATT | TTTGCTTTGA | ATGCTTCAAG | AACTGTTGGA | ACTGTTTCAC | CCGTCATGAC | 600 |
| TTCGCGCTCT | GCTTCTGTCA | ATTCCTGGGA | AATCTGAGAA | GAAAGATCTG | TCCATGGGAT | 660 |
| ATCTCATCTA | CTGATTCATT | GTGGTTTATA | GAG | | | 693 |

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CTGACAAAGG | AGACGGGTAT | GGAACAAACA | TTCTTTATCA | TCAAACCAGA | TGGTGTA AAA | 60 |
| AGAGGGCTAG | TGGGTGAAGT | GTTAAAGCGC | ATCGAACAAC | GTGGATTTAC | AATCGAAAAA | 120 |
| TTGGAGTTTC | GTTCACAGGT | TTTCAGAAGA | GTAGATTGAC | CAGCACTATC | AGGACCTGGT | 180 |
| TGGTCAGAGT | TTTACCCAC | CGATTCTGTA | ATTCATGACT | TCAGGTCCAG | TTCTTGTGGG | 240 |
| TGTCATTCT | GGTCCCAAAG | TAATCGAAAC | TTGGCGGACC | ATGATGGGTG | CAACTCGTCC | 300 |
| AGAAGAAGCT | TTACCAGGCA | CTATTCGAGG | TGATTTTGCA | AAAGCTGCTG | GAGAAAATGA | 360 |
| GATTATCCAA | AATGTTGTAC | ATGGTTCAGA | TTCCGAGAAG | AATCAGCTAA | GCCGAGAAAT | 420 |
| TGCTCC/TTG | GTTTAAAGAG | TGGATTGGCT | CAATCAATTG | GATAAAAGCT | CATTTGAATA | 480 |
| GAAAGTATAG | TCAATTAGTT | TAAGACATGA | CGCATGATAT | CAAAC TTTT | AGTTT TTGAT | 540 |
| ATGGTGCGTT | TTT | | | | | 553 |

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

CTAGAGATTT NCGAAGAGTA TTATTGTACT TTAAAGGTCT TGAGATAATT GTCTTTNCCT      60
ACTTGACCTT CGAAGGTTTT ACCATTTTCA AGGTAAGGAA GGTCATCGGA TACTGAAGCC      120
TTGACCTTGT ATATCTTGCC ATCAACTTTA AAGAAGTAGA CAGTGTCTCC CTTGATAACA      180
GCTGATTTGA GGTCTGCTAC TACTCCCTTG ATGCTTTCTG TCGTTGCATT GTCAATTTCA      240
AGGTCGTTTT TATTGGCATA CTTGCTGAGC ATCTCTTCCA CTGTAGTAGC AACGATAACA      300
TTTTGGTACT CGACTGCGTC TACCAGGGCG TACTCTTTGA CCAAGCCAGC ATTGTCCTTT      360
AAGCCCATGA TGTAAGAGG CTTGTCATTG AGGTTGATAA AGATTGGGGA AAGGTTGCTT      420
TGTAGGATTT CTCCTGAACA GCACCTTCTG CTGATTACAG GGCTGATTCT TCTGTCGCAG      480
AAGCCAAG

```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

TACAGCTATC GGGTCCGTCT GGTAGTTGGT CCTCAGAACC TTCACTGCCA CTTCTTCCCC      60
ATCTAAGATT AAGTCTTTGG CTAGGTAGAC ATCCGCCATG CCTCCTCGAC CAATCTGTTT      120
GACAATCCGA TAGCGTCCGG CAAAATCTT GCCGATTTGG ATCATTCTTC ATCTCCTCG      180
TTCATAGAAA CAAGGGCAAC CGTAATGTTG TCTAAACCTC CTGCATTGTT AGCAAAACGA      240
ACAAGTGTCT CCGTTTTATC TGCTAAAGGA ATATCACTGG TTACAATATC ACGAATCTCA      300
CTGCCTGAAA TCATGTTGGT CAAGCCGTCA CTATTGAGCA AGAGATAGTC ACCTGACTCA      360
AGGATAACTG TCCCAAATC AGGCTGAATT TCATCTTTTT GCCCAATAGA CTGGGTGATA      420
ATATTTTTTT GTGGATGACT TCTGCCCTCT CTGGTGTCAG TTGACCAGCC TTGAGCAATT      480
CATTAACCAA AGAATGATCG CTCGTCAACT GATGGTATCT TCTCCACGAA TCAAGCCGAT      540
ACG

```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

| | |
|---|-----|
| CTTTAAGGAA AATCAAATCT CTCATGCTGA TACCTCTCCT CATTAAATTA AATAGTAAAA | 60 |
| AAGATTCTAT CTCACTCCCT GATTATTACA AAACCATTGA AATATCACAA CTAATAGGCT | 120 |
| AGAATGGACA TAGTAAGATN TAGTAGATGA GTCATTCTAC TCAAATCCAC GTTAGAAAGG | 180 |
| ACTGCTATGC CAGACAATCT CGCGCTTCGC ATGCGCCCTA AAACCATCGA CCAGGTCATC | 240 |
| GGTCAGGAGC NTCTGGTCGG ACCTGGAAAA ATCATCCGCC GCATGGTGGA AGCCAACCGC | 300 |
| CTGTCTCCA TGATTCTATA TGGCCCTCCT GGAATCGGCA AAACAGTAT TGCCTCTGCC | 360 |
| ATCGCTGGAA CGACCAAGTA TGCCTTTCGA ACTTTCAATG CGACAGTTGA TAGTTAAAAA | 420 |
| GCGACTGCAA GAAATCTCGG AAGAAGCTAA ATTTNCTGGT GGTCTCGTCC TATGCTAGA | 480 |
| CGANATTCAT CGACTAGATA GACC | 504 |

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

| | |
|---|-----|
| CTAATAGAGG CGAAAAAATT TCAGGTCCTC CTTTGCTAGA TGATAATGAG GAAACTAAGA | 60 |
| TTTACCAAC CTCTTCTTCC CGTTTGGTT ATGCCAATCC TAAGGATCAT GGTTTTAGCC | 120 |
| AGGAAACCTT GAAGATTCAG GTCGAACCAT CTATTCATAA AAGCCGTCGT ATTGAAAATA | 180 |
| CCAAGAGAAA TGCTTTCAAT TCTAAGTTGA ATAAATCTT ATTTGCGGTC ATCTTTCTCT | 240 |
| TGATTTTGCT TGTTTTAGCA ATGAACTTT TGTAATAGAA AAGGAATTGA AATGAAAATA | 300 |
| GGAATTATTG CTGCTATGCC AGAAGAACTG GCTTATCTGG TCCAGCATTT AGATAATGCC | 360 |
| CAGGAGCAAG TTGTTTGGG GAATACCTAT CATAAGGAA ACCATTGCTT CTCATGAAAG | 420 |
| TCGTTCTTGT TAAAAAGTGG AATTGGTAAG GTCATGTCTG CTATGAATTG TGTGGCGAAT | 480 |
| TTTGGCTGAT CATTTCCAGG TTGGATGCCC TTATTAATAC GGGTTCAG | 528 |

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTAATAAGAC | TGAAAAGAAG | TCCAGCCAGA | TGTCCCTAAA | AATACAGAAA | AAACATTAAA | 60 |
| ACCAAAGGAA | ATCAAATTTA | ATTCTTGGGA | AGAATTGTTA | AAATGGGAAC | CAGGTGCTCG | 120 |
| TGAAGATGAT | GCTATTAACC | GCGGATCTGT | TGTCTCGCT | TCACGTCGGA | CGGTCATTTA | 180 |
| GTCAATGAAA | AAGCTAGCAA | GGAAGCAAAA | GTTCAGCCT | TATCAAACAC | CAATTCTAAA | 240 |
| GCAAAAGACC | ATGCTTCTGT | TGGTGGAGAA | GAGTTCAAGG | CCTATGCTTT | TGACTATTGG | 300 |
| CAATATCTAG | ATTCAATGGT | CTTCTGGGAA | GGTCTCGTAC | CAACTCCTGA | CGTTATTGAT | 360 |
| GCAGGTCACG | TAACGGGGTT | CCTGTATACG | GTACACTCTT | CTTCAACTGG | TCTAATAGTA | 420 |
| TTGCAGATCA | AGAAAGATTT | GCTGAAGCTT | TGAAGCAAGA | CGCAGATGGT | AG | 472 |

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTTTTAAATA | AGAAGAATCA | CACTCATTGC | TAAATGTGAT | ATAATATTGT | TCTCAGTCTC | 60 |
| AGCAGTGCGT | TGTGAAAAAG | CCATACTAAT | CCCTGATTTT | TCCGCATATT | CCATCACCTC | 120 |
| AAGTGTTTTA | CTCACTGAGC | CAACTTGATT | AGGCTTTATT | ACAATACCAT | CAGCACAATC | 180 |
| TTTAAACTGT | GAAATTCTTT | CTAAGTTTGT | TGCGTAAAAA | TCATCACCAA | AAACTTGTA | 240 |
| CTTTAGAGGT | TTTATCAATT | GAAATTTTCT | CCAACTATCC | AAATCTTCAT | CGGAAAATGG | 300 |
| ATCTTCAAGA | TAAACCAATG | GATACTTAAC | TCCCCAATCA | CAATAAGTAT | CCATAATTTT | 360 |
| TGTGACTGTC | TGTTGCTGAC | TAACACACCA | TGGTACTTTA | TATATGCCAA | GTGAAGAATC | 420 |
| GTAACGATCT | GTCATTGCTA | AATCTAAACC | GATATCATAT | CTATTTTGT | ATAATTTTAA | 480 |
| TGTCTCTAAT | AACGAATCCA | AAATAATATA | AAAATCATCC | GTGTTAATTA | TTAATGCACC | 540 |
| TTGATAGAAA | TAGATGTTGT | AGAAACCTGG | GTTTAACTT | TATCATAACT | CATTTTATG | 600 |
| TTAGA | | | | | | 605 |

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```

CTGAAGAAAA TCAGTAAACA AGAGCTGGTT AACACGCGCT TTTCTCGTTT ATTTGCTCAT      60
TTTGGACAGG AAAAAGACGG TAGTTTTCTT GCCCAGCGTT ACCAATTTTA CCTCGCCCAG      120
CAGGGACAAA CACTATCGGG CGCTCATGAT CTCTTGGACA GCCTCATTGA GCGTGATTAT      180
AACTTGATG CTGCGACAAA TGGCATTACT GCCATTGAGA CAGGACGTTT GGCTCAATCT      240
GGTCTAGCAC CTTATTTCAA TCAAGTCTTT ATCTCAGAAC AGTTGCAAAC TCAAAAGCCG      300
GATGCTCTTT TTTATGAAAA GATTGGCCAG CAAATTGCTG GATTAGTAA AGAAAAGACC      360
TGATGATTGG AGATTCTCTA ACCGCCGACA TTCAAGGTGG CAATAATGCG GGGATTGACA      420
CTATCTGGTA TAATCCTCAT CACCTCGAAA ATCACACACA AGCCGAGCCG ACTTACGAAG      480
TCTATTCTTA CCAAGACTTG CTGGATTGTT TAGATAAAAA TATTCTTGAA AGATCACGTT      540
TTAAGGAGAT AG

```

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```

CTTTGTCTGT ATCTGCCTTT TTATGCTATA CTTAAGGTAT GCATAGAAAA ACAGTGATTG      60
ATTNTAGGAC TTTAGGGGAG AGATATACCT TTACCCANCC TATTAAAGAG TTGAAAACGA      120
GAAATGTAGC AGAAGTGGA GATTGCTGG CACNAGTGGA AAGCTACCAA GAGCAAGATT      180
ATTATGTGGT GGGGTATGTC AGCTACGAGG CTGCACCTGC TTTTGAGGAG AAATTAGCAG      240
TTCACAAGGT TCCTCTACTG GCGAGTACT TGCTTTACTT TACTGTTTAC GATAGGGTGG      300
AGACCTCCCC TATTCCTCTG ACTTATGAGG ATATTGATTT GCCCTCAAAT TGGCAGGGAA      360
NTAACGTCTG CACAGAACTA TGANAAGGCC ATTGCCCAGA TACAC

```

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

| | |
|---|-----|
| CTCAAAAACA GCTTCTAACA GCTTGAACAA GGGGGCTAAA ATTGATTCTT TGATGTAGGG | 60 |
| TTTGAAGTAA GATAATAGGT GTTTCATAAA TCCCTTCTAT TCATATTCTA GAAATGAAGA | 120 |
| AAGTGGGAAG CCCCACTCTC TGTTTTATTT GTTTAAGTAA GGCAATAGAT AGCCATATCC | 180 |
| TGCTTTTTTC ATCTCATCCT TGGCCACAAA GCGTAAAGAA GCAGAATTGA TACAGTAACG | 240 |
| GAGGCCGCCT AACTCCCGCG GTCCATCTGT GAAAACATGA CCCAAGTGAG CACTGCCTGA | 300 |
| ACGAGAACGA ACTTCAATTC GCTCCATTCC ATGGCTCAGA TCCTTGTAAT AATGAATCAA | 360 |
| CTCTTTGGAA ATCGGACGGC TTAAACTTG GCCAACCCAC AACCTGAAGC AAACCTATCC | 420 |
| TTGGCAAAAA AGAGTTGGCT CACCTGTTCT TAATATCTAC ATAAATCCCC TCCTTCCAAA | 480 |
| GGTTTGGTTC CATAGGCATT GGTAAATGGA CCTCTGTGA CCAG | 524 |

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

| | |
|--|-----|
| CTTCATCTGG TGGTTCTCCA GTTGTAAAGTA ACGTAGTACC ATTCTCAAAA CCATACTCAC | 60 |
| AAGTTGGTAT TAAGGGGGAA CCATATATCT TTAAAGGAAT GAAATTGCAA AAAGATATTG | 120 |
| TTACAACAAA AGAATATAAC GAGGTTTAA AAAATGGCAA AAAGAAAAAT TGGAATCCAA | 180 |
| TAGCAAATAC CAAAAGAAC TAGAAAAATA CATTAATATA GGAATGGTAT TGATCTTGAT | 240 |
| AAAATTTTAA AAATACTGTC ATTTTGAATA TAAAGGAGTT TGATATGGAG TGGATTAGAT | 300 |
| TAATAGGAAT AGCAATCATT GTTGTGGGTT TTATTTTAAA ATTTGATACA ATTGCAACAG | 360 |
| TAGTCTTAGC TGGTTTGGTT ACAGCTTTAG TTTCAGGTGT TTCTCTCGTT GAATTTTGG | 420 |
| AGATTTTGGG AAAAGAATT AGCAATCAGC GAGTGCTCAC GATTTTATG GTTACCTTGC | 480 |
| CTCTTGTGGG GCTGTCAGAA ACCTTTGGAC TCAACAACGA TCAATCGATT TGATTGAAA | 540 |
| GATTAAAGGT CTGACAGTTG GAAACTTCTA TACAGTTTAT TCTTTATCGA GAG | 593 |

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

| | |
|---|-----|
| CCTGCTCCTT ATCTTTGCAG TAATTGGCGT TTTAGTGGCC TTGATAGCTC AATTTTACTC | 60 |
| AGCAAAGGCA GCAGTAGGTT TTGCTAAGGA ATTGACAAAC GATCTTTATC GTCATATTCT | 120 |
| TTCCTTGCCC AAGGACAGCA GAGACCGTCT GACAACTTCT AGTTTGGTTA CTCGCTTGAC | 180 |
| TTCGGATACC TACCAGATTC AGACTGGTAT CAATCAATTC CTGCGTCTCT TTTTACGAGC | 240 |
| GCCCATTATC GTTTTGGTG CCATTTTAT GGCTTATCGA ATCTCAGCTG AGTTGACTTT | 300 |
| CTGGTTCTTA GTCATGGTTG CCATTTTGAC CATTGTCATT GTTAGGGTTA TCTCGATTGG | 360 |
| TCAATCCTCT CTACAGTAGT CTCAGAAAGA AAACCGAACC ACTGGGTTCA NGAAACCCCC | 420 |
| CNCCATTGCA AGGATGCCGG GTTATTCGGT GCCTTT | 456 |

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

| | |
|--|-----|
| CTTGACAGT TGAATCGTTC AGATATTGAT TTTGAAAACA GAGAGTGTGT TGTCTTTGGT | 60 |
| AAAGGAAAGA AGGAGAGACC AGTATATTTT GACGCTCGGA CGAAAATTCA TTTAAGAAAT | 120 |
| TATCTTAACG ACAGAAAAAG ATAGTCACCC TGCTCTTTTT GTAACGCTAG TTGGAAAAGC | 180 |
| CCAGAGACTT GGAATTGCTG GTGTAGAGAT TCGCTTAAGA AAGTTAGGAG ACAAACTCGG | 240 |
| CATACAAAAG GTTCACCCAC ATAAGTTCAG AAGAACTTTA GCGACTAAGG CAATTGATAA | 300 |
| AGGTATGCCT ATCGAACAAG TCCAAAAACT GCTAGGTCAT AGCAAGATTG ACACAACCCCT | 360 |
| GGCCTATGCC ATGGTCAATC AAAATAATGT CAAGCATTCA CACCAAAAAT TCATCTCTTA | 420 |
| AAAGCAAATC CCGATATTCC GAAGAGGTGG TTGCATGAAG AAAGTGAAAT TAGGTGAAGT | 480 |
| GGCTACTTTT ATCAATGGCT ATGCTTTTAA ACCTCAAGAT TGGTCCTCTG AAGGAAAGAG | 540 |
| ATTATCCGAA TTACCGAATC TGACT | 565 |

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

| | |
|---|-----|
| CTTTATACTT TATCATTTCT AACTTAATTA TAGTCTTATT TTAAATAAAG TTCAATTATT | 60 |
| TATATGTAAA ATTCCTCATC AGTAAAAAAT AACCGATCTC ATTTCTGAGA ATCGGTTTTC | 120 |
| TAAATAAATC AAACCGATCA TTTACATAAC ATAAATTATG TAAATGATCA TACTACAACA | 180 |
| ACAAATCTTT GACTTTTCCA ATTTCACTTT TTGGAATAAC CAGGTGAATC ATATCACCCA | 240 |
| GATACATTCT GGTGAGCCG TTAAGTGTG GGCTCTTGCC ATTATGGACT TGAGTTGTGA | 300 |
| TGAGGACGTT GTGTGGTAAG TTGAGTTCAT GAACTTGTTT CCCAGCAATT TTATCAGAAA | 360 |
| CTGGTATTTT GATAAGTGTA ACTTCTCCTT CGCTAGATAC TTCTTCTGGG AAGCATTTTT | 420 |
| TCCAGCATGG CTTCATAGAC TGGCGTTCCT TTGAGCNAAT CCCTGATNAT TTTAGAAACC | 480 |
| AGAGTGACAG ACCAGTGGCT TAAGGTGCGA ATATCTCCTA CCATCTCAGT TACGAGAT | 538 |

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

| | |
|--|-----|
| CGTGCTAACC ATGAGAGCAT ATATTTCTCT CAACTATTTC TATTTCAAAA AATCCTTACT | 60 |
| ATATTGTATC ACAATCAGAC ACAAAAAGAA AAAGCAAATG ATAAACAAAT GCTTTTAAAG | 120 |
| TTTTAAAAAA AGCTTCGAAA GGTCTTCTTT TATTTTAA NGGGAGAGAT AACGTTGATA | 180 |
| TCTAAATCGT GGTCAAAGCC GGCAATTTTC CTTTAGATGT GTATTGGTGA ATATCATAAT | 240 |
| CTAAATCAGT TTTAGGACTG CTCTCCAAAA ATCCTGAGTC TGAGCCGTAG GACGGAATCC | 300 |
| AAACAGAGGT AAAGTTGCCT GTATCAATAC TGTGTTCTTC CATGAAGTAG ACACCAACGT | 360 |
| AGATGCCGAT GTTTTATGCA CCTAGTGATG CTAGTTTTCG TCGAAAGTTT TCGACACCTT | 420 |
| CGTTCATATA GACATAGTTT TGTCTCCACG TCAGCCCATTA GTAAGTAGGC TGTTAGGAGA | 480 |
| GCACATTGTA GAAAACTTCG GCAGCCTTT | 509 |

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

CTGTTCTGTT TCGCAGCCTA CTTGGTTGTA GCATGGGGGT GGTTTTAGAT GGTCAGTAAG      60
TATCTTTTAT TAGCAGTTAT TTTCTCTGGC TTGGTGACTT GGATTCTCCG TATGATTTC      120
TTCATCTTAG TCAAGTATAA GGGCTTGCCT GCAATCGTTG AGCGTTTTTT GAAGTTCTTG      180
CCCGTTTCCA TTATCTTTCG CTTGATTCTT TCAAGCGTAG TGACAGGTAA GGTTGGGAGC      240
CTTCCTCAAA TTAAATGGCT AGACTTCTTA GCCGTCTTTC CAACAGCTTG GGTAGCCTTT      300
CGCTACCGCA ATCTACTCGG AACAGTTCTC TTTGGAGTGG TCTTGATTGC CATCTTGCCT      360
TTGGTCTCTT AAATTACCCA CCAAAAAAAC TTATCACAGA GATAGATATC ATATAATGGC      420
GTAAATGCTC CTTTCTGTT AAGATTATAA GGTATTCTAT TTGGAGGAA ATGACATGAA      480
AAAAATCGTT AAATACTCAT CTCTTGCTGC CCTAGGACTT GTTGCTGCAG TGTGCTTGCG      540
GCTTGCTCAG GGGTGCTCAG AAAGAAGAGA AC                                         572

```

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

CTAGGTTATT TAGTAAAAGA CTAGAAGATT TTCTTTTCCC AATCGTCTTC TGTACGGCGA      60
GGATAGAAAA ACTCTGACTT GTCGGGAGCT TCCATCATTT CCATCAATGG TAGCATATCA      120
TAGGCCAGAT TTAAGTTTGG AATCTGGTCT TTTGACACC AAGAACTTC TCCCTCTTCT      180
GAAGATTGAA GGGTACCAGA GAACTCAGTC GCCTTATAAC AAATGACAAT ATAGCGCCCA      240
CCTGTATCTA GTGGCCAATT TTTAATGCCG ACAAGTTGAG GATTTTGAT AGTCAACCCT      300
GTTTCTTCGT AGATTTACG AATGACAGAC TCCGAAAAG CCTCATCATT TTCTACATGA      360
CCTCCAGGAA AGGCATAACC AGACCACCGA TTGTTTTAG GGGCGCGATA CTGCATCACC      420
ACGCGCTGAG TTTCGANGTC TTCCATCAGA CAGATATTG TTAAATTGT TTAATTGGGA      480
ACGGGACATA AATTAC                                         497

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(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

| | |
|---|-----|
| CTGAAATTTT GGAAGAAGAA ATCGGTGTAG ATACAGTCCA AAAAATAGGA CGCATCTTGA | 60 |
| TTTTGTTTAA ACAATCTAGC AAGAAAGAAA ATCGCAAGAT TTCTAAGAAA GTCAAAGAAA | 120 |
| TCTAAGATCG AAACCTCCAA TAACGTGTTT TATAGAGAAA TAAAGGGGAC TAGCCTATGA | 180 |
| CAATCGAACT ATTGACTCCC TTTACCAAGG TAGAGTTGGA GCCAGAAATC AAGGAGAAAA | 240 |
| AACGCAAACA AGTTGGGATT TTAGGGGGGA ATTTTAACCC TGTTCACAAT GCCCATCTCA | 300 |
| TTGTTGCGGA TCAAGTACGG CAACAGTTGG GACTGGATCA AGTTCTGCTC ATGCCTGAAT | 360 |
| ACCAACCTCC TCACGTTTGA TAAAAAGGAA ACCATCCCTG AACACCATCG TCTCAAGATG | 420 |
| CTTGA | 425 |

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

| | |
|---|-----|
| CTGCTATCAA GACAGTATTA CCGCTGAAAG AAACAGCTTC ACTAGAAGGC GCAATTGAAA | 60 |
| AATAAGACGG GATCACGAAC TCCCGTTTTT CTATAAAGA AAGGAAATGG GATGAAAAAA | 120 |
| TTAGTCTTTG TCTGTCTGGG AAATATTTGC CGTAGCCCTA TGGCCGAGTT TGTTATGAAA | 180 |
| TCAATGACAG ATAACACGA AATCCAAAGT CGAGCAACTT CCTCTTGGGA ACATGGCAAT | 240 |
| CCGATTCATA AGGGGACTCA GGGAAATTTT CAAGAGTATG AGATTCCTTA TGACAAGAAC | 300 |
| AAGACATCGC TTCAGATTAG TAAGGAAGAT TTTGAAGCCT TTGATTATAT TATCGGAATG | 360 |
| GACGCTTCAA ATGTTCCGAC TTACGTCAGA TGTGTCCAGT AGACTGTCAA GATAAGAT | 418 |

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTGTTTGAA | AAATATGATT | CGTGGTCGAG | AAATGAATTG | CATTTAAGCA | ATGTAGTTCA | 60 |
| GTATATAGAT | TTGGAAATTA | ATGATTTAAC | AAAATAAAGG | AGAAAAACA | TGGTTAAATA | 120 |
| CGGTGTTGTT | GGAGCAGGGT | ATTTTGGAGC | TGAATTGGCT | CGCTATATGC | AAAAGAATGA | 180 |
| TGGAGCAGAN | ATTACTCTTC | TCTATGATCC | AGATAATGCA | GAGGCGATTG | CAGAAGAATT | 240 |
| GGGAGCAAAA | GTTAGCAAGT | TCCTTAGATG | AGTTGGTTTC | TAGCGATGAA | GTTAGATTGT | 300 |
| GTTATCGTCG | CAACTCCCAA | ATAATCTTCA | TAAGGAACCG | GTTATTAAGG | CTGCACAGCA | 360 |
| TGGTAAAAAT | GTTTTCCTGT | TGAAAAA | | | | 387 |

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTTATGAAAT | CAATCATCAA | AATAATATTG | ATCAGGACTA | TTAGGTAAA | TTATCTACAA | 60 |
| CGATTAAATT | GGTAGCAGAA | AAGGAAAATG | CCGTTGAGAT | CCTAGAACAC | TTGAATGTTG | 120 |
| TCCCTGTGTT | GACAGCCCAT | CCAACACAAG | TGCAACGCAA | AAGTATGTTG | GATTTAACAA | 180 |
| ATCATATTCA | TAGTCTTTTG | CGTAAATACC | GTGATGTAA | GTTGGGGTTA | ATCAATAAAG | 240 |
| ATAAATGGCA | CAATGATTTG | CGTCGTTACA | TCGAAATTAT | CATGCAGACA | GACATGATTC | 300 |
| GTGAGAAAAA | ATTAAAAGTG | ACTAACGAAA | TCACGAATGC | TATGGAAATA | TTACAACAGC | 360 |
| TCCTTTTGA | AAGCTGTCCC | TCATTTGACG | ACGGAGTATA | AGCGCTTAGC | GCAAGCGCAT | 420 |
| GGTCTGAATT | TAAAACAGGC | TAAACCAATC | ACCATGGGTA | TGTGGATAGG | TGGTGACCGT | 480 |
| GAAGGAAATC | CATTTGTTAC | AGCAAAGAAC | TTGAAGCAGT | CTGCACTCAC | TCAGTGTGAA | 540 |
| GTCNTCCTGA | ACTTACTATG | A | | | | 561 |

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

| | |
|---|-----|
| CGACCTAATC ATATTGATAC TGCATTTGCA TCAGCAGATT TGTTTGAGTA TAAATTACAA | 60 |
| TTAGCAGGAC AGACTTGGGG ATATTTAGAA TTTGAAACAA ATACAGAAAA ATATGGGAAA | 120 |
| GTATTGTTAA TTATAAAGGG TAAGAAGCGA CTTACGAACC AATTCCTTT GGTACAAAAA | 180 |
| AATAAGAGTG GCTACTTATT TGAATATGCT CAGATGAATA CACTTTATCT TAATCAACAT | 240 |
| TCTTCCTACA AAAATGATGA AGATAGTCAT TCCTTTCCAA TTCAGATGGA GTTAGTTTCT | 300 |
| GATGAAATGA TTCCAAGAAA TTGAACAAGC TACTAAAAAT TCCGAATATC CGAAAAATTT | 360 |
| ATGATTTTAA CTTATGANGC GGACTCCCGA AAAACAATAT TATATCTGTT AGATGTTTGT | 420 |
| TATGCCCTGA TGCCCGAACT GGTCCAGTTA CACTTGATT CAGATTGTCC TGAGTATATC | 480 |
| CATCCAGTTC CGTACC | 496 |

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

| | |
|---|-----|
| CCACCCTCTA GCAAGTGGTG CTAATTCCTA TAGCCTAGAA GAAAACGAAA TCATCTACCA | 60 |
| AAAGTTAAAA AACTTGCTTA AAAACTGATA AAATACTTGC CAAACTTTTC AGAATCTGAT | 120 |
| AGACTAGTAT GGTAACAATC TATGGCTCGC AAAGAGACCA TGGCAGAAAG GAAATATTGC | 180 |
| AAAATGAAAA AAGATATCCA TCCAGAATAT CGCCCAGTTG TCTTCATGGA CACAACACT | 240 |
| GGTTACCAAT TCCTTAGCGG TTCAACAAAA CGCTCTAACG AAACAGTTGA GTTCGAAGGC | 300 |
| GAAACTTACC CATTGATCCG TGTGGAAATT TCATCAGACT CACACCCATT CTACACTGGA | 360 |
| CGTCAAAAGT TCACTCAAGC AGATGGACGC GTGGATCGTT TCAACAAAAA ATACGGTCTC | 420 |
| AAATAATGAT AAGAGAACAG TTTCGGCTGT TCTTTTTTGT TTCTTGAAAT CAACTGCTGT | 480 |
| TTTCATGTTT CAGACTCATC TGTA | 504 |

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

| | |
|--|-----|
| CTCAGGCGAT TACTAATTAC ATGACTTCTG CCTCAAACCTT TAATGTCGAT GAGGCTAGCC | 60 |
| AATTCATTCA ACAATTTACA ATTACAAAAC AAATCGAACA AGTAGAAAAA CTATTAGAGG | 120 |
| AGTAGCATGG AACTGCATT AATTAGTGTG ATTGTGCCAG TCTATAATGT GGC GCAGTAC | 180 |
| CTAGAAAAAT CGATAGCTTC CATT CAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT | 240 |
| GTTGATGATG GTGCAACAGA TGAAAGTGGT CGCTTGTGTG ATTCAATCGC TGAACAAGAT | 300 |
| GACAGGGTGT CAGTGCTTCA TAAAAAGAAC GAAGGATTGT CGCAAGCACG AAATGATGGG | 360 |
| ATGAAGCCAG GCTCACGGGG ATTATCTGAT TTTTATTGAC TCAGATGATT ATATCCATCC | 420 |
| AGAAATGATT CAGAGCTTAT ATGAGCAATT AGTTCAAGAA GATGCCGATG | 470 |

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

| | |
|---|-----|
| CTTATACTTG CTTTTTCCT TTTGAAAAAT GTTAATAAAT CGTTGGTAGT CTTCTCTAGG | 60 |
| CATGGACAGA TCAATATCGT CGTCCCAAGG GATAAAGCCC TCATGTCGAA CCGCCCCAAT | 120 |
| CAGAGTACCG TAGTTAATAA TATAGTTGAT ATTGTGCTTT TTACAGAGAG TATCAATATA | 180 |
| ATCCAAAATT TCTAATTCAA TTGTTTGGC ATCTTCAATG GTTAGTTGTT TCATTTTAAA | 240 |
| CTCCTATGAT TTTTGAATT TATTTTAA GGCTAGGACA TGGTTTAAAA ATTCATAGAA | 300 |
| AATGCTATCT TTTGTGAAGA CAAGTAGACT AATATAAGAG ATAGCTGATA ACAAGACAAT | 360 |
| CAAACCAAGTA TTAATCAAAA ATGGCAAAT AATGACCATA TCCACAGGAT ACACGAAATT | 420 |
| AATCAGGAAA TACATTGCTA CAAAGGAAAG TGAAAAGAGA GAGTATCGAA CAGTATAGCT | 480 |
| AAAGATATGT CCAAGTGGA TGAGTTGTT CTATGGATGA AATGAT | 526 |

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

| | |
|---|-----|
| ACCATATCAA TACTATCGAA AAGTACAAGG GATNCAGTCT CAAGGTCGCT GAGGAAGATT | 60 |
| TGAATGACCT AGACGATGGT GAATTTTACT ATCACGAGAT TATCGGTTTG GAAGTCTATG | 120 |
| AGGGTGATAG CTTGGTTGGA ACCATCAAGG AAAATCCTGC AACCAGGTGC TAATGATGTC | 180 |
| TGGGTGGTCA AACGAAAAGG CAAACGTGAT TTGCTTTTAC CTTATATCCC ACCAGTGGTT | 240 |
| CTCAATGTTG ATATTCCAAA TAAACGGGTC GATGTGGAAA TCTTAGAAGG GTTAGACGAT | 300 |
| GAAGATTGAT ATTTTAACCC TCTTTCCAGA GATGTTTCT CCACTGGAGC ACTCAATCGT | 360 |
| TGGAAAGGCT CGAGAAAAG GGCTCTTTGG ATATCCCAGT TNTCATAATT TTTCAANAA | 420 |
| AATGCTGAAA AGG | 433 |

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

| | |
|--|-----|
| CTGCAACTTG AATTTCTCCT TCTTGTTTCA AAGCAAGATA AACAAATCGA GCCCCCTCTTT | 60 |
| TTTCTAGCAA ATCCCCCATC TGGACAGATT GCATAAAGGA ACGAGAAGAA ACCTGATCAG | 120 |
| AATAAGTCTG AAACCTTCTT TCGTGAGTG TTGTTAGTGC CATATACTTA CTTTCTATGT | 180 |
| TTTTTTCTTA ATGTTTTTACG GAAATCAAGA GCAAGTCTTA ACAGAGGATA GAGAGGATGA | 240 |
| GTGGGCATTG TAAATTCACC CAAGTATTCT TCAATCGTTG GATTAAATTT TTCTTAAAA | 300 |
| TGATAAAGTC CACCATTGAG AGAGTTTTC AACCACCTA AATTTTGCCA GACCATACCT | 360 |
| CGCTCAAAGG CATAGCGAGC CGTTTCATAC CATGTAAAAA TTGGTGCAAT GTAACGTTTA | 420 |
| AAATCATCAT CCATACCAGC ATATATATTG ACAGAGGTAG TACCAAATTC CAAACTCAAA | 480 |
| GTACCGCTAA AGGAATCTCG CTTGACCTAC ATCTATATAT TCCTGCAAGA AGGTCAATTC | 540 |

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

| | |
|---|-----|
| CTCAGGCTAA AAGAGTCCAC TGGACTCTTT TACTCCGTCC CATAACCAAT GACTTAATGG | 60 |
| CGCGTTCAGC TAGATTATTG GAAAGGACCA GATGTCCGTC TTTCAAAATA GTCTTAAAGG | 120 |
| TTTCTTCATA CTTGAGGCTG TATTCAATTG CCCTTCCTAG TTTTGAACCC GATAAAACTG | 180 |
| ACTGACGCCG GCACCAAGCA AAGAAATCTT CCATTAGGGG TTGGAGCTCT TCTTGACGTT | 240 |
| TCTGTAGTCG TTCATCAGCT GACAATGTCT CCCAGTCTCT TTCCAAGGCA AATAACTGAT | 300 |
| CACAATAGGC TAATCCTTTA G | 321 |

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

| | |
|--|-----|
| CTTGACCAAA CAAGGCAGTT GGAAATTGAT TTTGGAGGAT GAGAGCGCTG GAAGGGAAC | 60 |
| CTTCCCAATC TTGACTCAAG GTCNATATAT CGCAACATTT GACCAACAAG CGCCANCTAT | 120 |
| CGATGAAATC TTAAACTAT AATCAGGAGT GGAAGTATGA GAAATATGTG GGTGTGAATC | 180 |
| AAGGAAACCT ATCTTCNACA TGTCGAGTCA TGGAGTTTCT TCTTTATGGT GATTTGCGCCG | 240 |
| TTCTCTTTT TAGGAATCTC TGTAGGAATT GGCATCTCC AAGGTTCTTC TATGACTAAA | 300 |
| AATAATAAAG TGGCANTACT GACAACAGTG CCATCTGTAN CATAAGGACT GAAGAATGTA | 360 |
| AATGGTGTTA ACTTCGACTA TAAAGATGAA GCAAGTGCCA CCAGAAGCAA TTAAA | 415 |

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

| | |
|--|-----|
| CTATNAAATA GAGTGGTTCT CTATCTGCCA TGACCACAAA TNAGGACAAT GATACTTCTG | 60 |
| AACGTTTCAGA CTGCTATCGT AAAAGGACAG CGGGTGAGAC GCCCATGAAT GATCTAACCA | 120 |
| GTCATACCCA CGGAGGAAAT TATACAATAG CACGTTATCA GGAGGAAAAA TTTTGAACA | 180 |
| AACAGTTGTA AAATATAGTC TGCAGTTATC AATGCTTAAT TTTTACAGG CGAAGATAAT | 240 |

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

```

CTTGTATCC TCACGAAAAT TCGATTGTA AAGCACCAAG CCTTGACTCG TGATAGACTG      60
AATCATGCTT CTCTCATGTA CTCCTCAAGT CGTTTCATGG CTTCTTTGAT AGTCTCCATG     120
CTGGCTGCAT AAGATAGGCG GACGTAGCCT TCCCCGTAAC GTCCAAAGGC TGCACCAGGG     180
ATAAAGGCAA CGGCCTTCTT CTGAGCAAAA TCCTTCAGAA AAGCAAAGGA GTCTTGATTG     240
TAGCCCGCTG GAATTTTAGC AAAAATATAG AAGGCACCGT CTGGTTTGAT AATCTCAAAA     300
CCAAGAGCAG TCATTTTTTC GATGATATAG TCCCGACGTT GGATATATTC CTTCTTCATG     360
GGCTCCGCAT CGTTTTTACC AGCCGTCAAG GCTTCTACCG CAGCATGTTG CGCCATGGTA     420
TTTGCGGCAG TGACCAAGTT ACTGGTGACT CTTGATTAAC TGGGCTGTGA AGGTCNCANG     480
AGCAAAAATC AGCCCCAAAC GCCAACCTGT CATGGCATG      519

```

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

```

CTTCAGCTAT TCGTGGGATA TTAGATGTAC TTATTTAGGG GTTGAAATCA TATGAATATT      60
ACCAATTTGT TTTCTATCAA GACAGGATGT GATGAACTG ATAGGCAACT GCAAAAACATA     120
TTTTTTTCAGT TGGATTTACA ATTGGGAGAA TTGACAGATC AACTAAGAAA ATTAGATTCT     180
AATTTTGTTT CTCGTAGTCA ATTTGTAGAC ACGTTGGATT TGAATGATGT AGAATATAAA     240
GAAATTTTAA ACTATTTTAT CTTCCATCGT AATGATAGTG AAGAAAGTTT GGTAGAATGG     300
TTATATGATT GGATTTCAC AAATCGTTAT GAACCTCCCT AAAGAGTTTT CCGATTCCGT     360
ATGGCTCCAT AAATACCCAT GAAAGTGTTA CTGAAGTTTT CCGAGAATG AATAACTAAA     420
AAACAGTCAT TAGTGACTGT TTTTATAGA AAAGAGTTTT TATATGTT      468

```

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```

CTTGAATAGT CTCATCACGA AAATTGCCAT AACTGATAAA ACCAACCACC TTCACGCCAT      60
CCATCGCAAT CAATGTATTT TCTGGATACT TTTGACTAAA GAATCGACAT CTTTCTAATG     120
TCATTGTATC CTGAAATTCC GCAGGCAAAA GGTCATCATA AGACTCTCTC CACGTTTGCC      180
AGTGAACGAG GGATTTGCCT TCTATCTCTT CAGGAGTTNC CATAGATTTG ATAATAACCG      240
TCATTTATTT TCTCCAGTC TNCTCTCAA ATACCATATT TAATACTATC AAAATATTTA      300
CCTTGATAAT AACGAACTTT NGGAATATGA GCTNCTTTT TCATNCTTAA TTTTTCAGCA      360
AGTTTCATCA TACCAAGATT TCCTGACCAA GTTGTCAAAA CCAGATGCTC CAACTCCAAG      420
TAATCCTGAA ACGTCCTATC TATCCACTGC AACATAGCAA CTTTCCCAAT ACCAGTGTTT      480
CAGAATTTT TATCATAAAT ACCAATTCCC AATCCATCCA TCTTGTTTCC TTTACATACC      540
CAATA

```

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```

CTTGATTGTG GAAGAAGTCC GTGATCGCTA TGTGGGCAA GTCGATGCCG TTTTTCATAA      60
CGGCGATTCT GAACTACGTC CGGATTCTCC ACTTTGGGAG GGCATCCGCG TTGTTAAAGG     120
GAACATGGAC TTCTACGCCG GCTACCCAGA ACGTCTGGTG ACTGAGCTTG GTTCGACCAA      180
GATTATCCAA ACTCATGGTC ACTGTGTTGA CATCAATTTT AACTTTCAA AGTTGGACTA      240
CTGGGCTCAG GAGGAAGAGG CCGCTATCTG CCTCTATGGT CACTTGCA TGCCAAGTGC      300
TTGGTTGGAA GGCAAGATCC TCTTCTCAA TCCAGGCTCT ATCAGTCAAC CACGAGGTAC      360
CATCAGAGAA TGTCTCTATG CTCGTGTGGA GATTGATGAT AGTTACTTCA AAGTGGACTT      420
TTTGACACGA GATCACGAAG TGTATCCAGG TTGTCCAAGG AGTTTAGCCG ATGATGCCAA      480

```

GGAGTTGAGA CTTTCTGTTG GGGCAGAGAA CTTTGA

517

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

| | |
|---|-----|
| CGTAACCATT AACTATGAGG TGGTTTGCCT CCTCAGCGAC CGTATTCCGA GAGAATATTA | 60 |
| TTAGAAAAGA AAGGAGTGGA GCATGAATCT ACATCAACCC TTGCATGTCT TGCCTGGTGT | 120 |
| GGGACCAAAG TCAGCAGAAA AATACGCCAA ACTAGGAATT GAAAACCTGC AAGATCTCTT | 180 |
| GCTCTACTTT CTTTCCGTT ATGAAGACTT CAAAACCAAG CAGGTGCTGG AACTAGAAGA | 240 |
| CGGTGAGAAG GCAGTTCTTT CTGGTCAGGT AGTGACTCCT GCTAGTGTCC AGTATTATGG | 300 |
| TTTCCAAGCC GCCAATCCGC CTGCGTTTTT AGTCCTCCAA GCCAGGGAAG AAGGTTCGTT | 360 |
| TTTTTTTGGC GGGTGAAATT TCCTTTTAA CCCAGCCCCC TATCCTGGG CTTGAATAAA | 420 |
| AAATTAGAAA TTTTGGGGAA CCAACCCCTT TGGCTTGT | 458 |

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

| | |
|--|-----|
| CCTTACTAGT TTAATCAATC TTTACATCGT TCTTCGGCA GTTCAAACCTC AGAATCCACA | 60 |
| GCACAGGTGA TGCAATTACT GTCTGAAAAT ATGTTAAAAA CCATTCAGTC ACTTTCGGTC | 120 |
| TGGCAGATTT ATTTGCTTGG TTTTGAGCGA ATCTTGGCGC TTGGTTTCCA ATTACTTTTG | 180 |
| ACAGTTTGGG TTTACCAAGC TGTTCCGCCAG AAGAAATGGA TTTATCTCCT AGCAGCCTAT | 240 |
| GGCTTGCATG CCTTCTTTGA TCTGGCACCA TCTCTTTTCC AAGTAGGCTG GTTGACAAAT | 300 |
| CCAGTCTTGG TTGAAAGTAT TCTAGCACTG CAGCTCGTTC TGGTCGCCTA TGGAACCAAG | 360 |
| GAAATCTTTT GTAAAAAATC ATAAAAAGGG GGGAACTCTT TTTTCTTATG CAAAATCCAA | 420 |
| ACAAGGTAAT TTTATGGTCG TCAAAATGCT CTAATAATGG TATAATGGAA TGAATTTTGT | 480 |
| AAAAGGAAGA ATGACATGTC TGTAAGAGAA AAAATGCTTG AAATCTTAGA AGGAATTGAT | 540 |

ATCCGTTTTA AGGAACCCTT GCATAG

566

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

| | |
|---|-----|
| CTTTGACAAA GAGTATGACA CCTGACCGTG AAGTCATTAC CTTTATTCCT GAAAAATTTA | 60 |
| TTGTGGATGG TTTCCAAGGG ATTCGTGACC CACGTGGCAT GATGGGGGTT CGCCTTGAAA | 120 |
| TGCGTGGTTT GCTTTATACA GGACCTCGTA CTATCTTGCA CAATTTGCGT AAGACGGTTG | 180 |
| AGCGTGCAGG TGTTCAAGTT GAAAATGTTA TCATTTACC ACTAGCAATG GTTCAGTCTG | 240 |
| TTTTGAACGA AGGGGAACGT GAATTTGGTG CTACAGTGAT TGATATGGG GCAGGTCAAA | 300 |
| CGACTGTCGC TACAATCCGT AATCAAGAAC TCCAGTTCAC ACATATTCTC CAAGAAGTGG | 360 |
| AGATTATGTA ACTAAAGATA TCTCCAAGGT TTTGAAAACC TCTCGCAAAT TAGCGGAAGG | 420 |
| CTTGAAACTG AATTACGGGG AACCTATCCG CCTCTTGCAA GCAAAAACT CCATTAAAGT | 480 |
| TATTGGAGAA TTAAACCAGT CAAAGTGACG GAACCTACTT GTC | 523 |

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

| | |
|---|-----|
| CTGTGATTTT AGAGAAGAAA TCAAGTGCTG TAACAGAACT AAGATGTAAT TGTATGTAAA | 60 |
| GGAGACGTCA TGTAAATAG TATTGTAACC ATTATTTGTA TTGCCCTTAT CGCGTTTATC | 120 |
| TTGTTTTGGT TTTTCAAAAA GCCTGAAAAA TCTGGACAAA AAGCCCAGCA AAAAAACGGA | 180 |
| TACCAAGAGA TTCGAGTGGG AGTCATGGGA GGCTATACTC CTGAGTTGAT TGTCTCAAG | 240 |
| AAATCAGTGC CAGCCCGCAT TGTCTTTGAC CGCAAGGATC CTTCAACATG TCTGGATCAA | 300 |
| ATTGTTTTTC CAGATTTTGG TGTACATGCG AACCTGCCAA TGGGGGAAGA GTATGTAGTG | 360 |
| GAAATCACGC CTGAACAGGC TGGAGAGTTT GGCTTTGCTT GTGGTATGAA CATGATGCAC | 420 |
| GGCAAGATGA TTGTAGAGTA GGTGGAGACT ATGACAGAAA TTGTGAAAGC AAGCTTAGAA | 480 |

AATGGCATTCC AAAAAATCCG TATCCGAGCT GAAAAAGGCT ATCATCCACC CATATCCA

538

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

CCTCAAGAAG TCCGCGATAC TTACGAAAAT ATTTTGTAGA GAATCGAACC GCAAGGTTTC      60
GTTTTCTTTC TCTTTTGTGC TATAATTTGG TATAATAAAC AGTATGAAAA TCGTATCAGG      120
AATCTATGGG GGACGTCCCC TCAAGACACT AGAAGGCAAG ACAACAAGAC CTACTTCGGA      180
TAAGGTTAGG GGAGCCATTT TTAACATGAT TGGTCCCTAC TTTGAAGTGG GACNAGTCTT      240
GGACCTTTAT GCAGGTAGTG GTGGTTTATC TATCGAAGCA GTATCGCGTG GCATGTCCAG      300
TGCTGTTTTC GTGGAGCGAG ACCGTAAGGC TCAGACCATC GTGGCTGAAA ATATCCAGAT      360
GACCAAGGAA GTTGAAAAAT TTCAACTCCT CCAAAATGGA TGCAGAAAGG GCATTGGAAC      420
AGGTTNTCTG GGGAAATTGA CCTCGTTTTC TTAGACCCTC CCTATGCCAA GGAACAAATC      480
GTAGCAGATA TTGAAAAAAT GGCTGAGAGA GAGCT                                     515

```

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```

CTGGANACAA ACTTTACAGA TCAAGTCGAT ACGATGATTT ATGTTGATAA AGAAGAAAAA      60
GAAACTATTA AAGCTGCACT TGTGGAGTTT TTAAATGGAA AAGTCACTTT AACTGACCAA      120
GGTTTACGAG AGGTTGAAGT TCCTGTAAAC TTAGTGATAA CAATGAATAA TACAGCGTTT      180
CGTTGACATT CTCACAACTA CTTTAGCGAG CAAAATAAAA AGATGCGTAC CAAAATATAC      240
TAGAAAATGA AGCAATTCAA ACGAAACCTG ATATCGTTTT CCTTCACACC TATTTACTAG      300
AATTAAGTGA ACGCAATCAC TTGAAAATTA ATGACTTTGG AT                                     342

```

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

| | |
|--|-----|
| CTATTAGCGA CTTTCTCTGA AATATGGTAT GATAAAGGAT ATACAAGGAG ATAAAAATGAA | 60 |
| TAATAATTTA CTGGTATTAC AATCCAGACT TTGGTCTGGT TGATGGTGCG GTATCGGCTA | 120 |
| TGATTGGAGT GGCTTTAGAA GAGTCTCCAA CCTTAAAAAT CCATCACTTG ACGCACGATA | 180 |
| TCACGCCCTTA TAATATTTTT GAGGGGAGCT ATCGTCTCTT TCAGACGGTG GATTACTGGC | 240 |
| CTGAGGGAAC GACGTTTGTA TCGGTTGTCG ATCCAGGTGT CGGTTGCGAA CGTAAGAGTG | 300 |
| TAGTTGCCAA GACTGCTCAA AAATCAATAC ATTGTCACGC CAGATAATGG GACGCTTTCC | 360 |
| TTTATCAAGA AACACGTTGG CNTTGTANCC ATTCGTGAGA TTTCTGAGGT GGCCAACT | 418 |

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

| | |
|---|-----|
| CTCTCGCTTT TCTCATAGTG GGAGGTAAGG ATGGAATTAC GCAGACCAAG ATTAGCGGAT | 60 |
| AAGAAAGCTG TTTTAGATAT GATGACAGAG TTTGAAAAGA GCCAATCAGC CCATGATGGA | 120 |
| GGATTTTGGG ATACAGAGAA TTTTGTGTAT GAAGAGTGGT TGGAAAGCAA TCAGGAACAG | 180 |
| GAAATGGGGA TTAATCTGCC TGAAGGATGG GTTCCTGCAA TTCAGTTAGT GGCTTTTTCT | 240 |
| GAGAAAGGTC AAGCAGTTGG ATTTCTTAAT CTCCGGTTGC GCCTCAGTAA CTTTCTACTA | 300 |
| GAAGAAGGTG GGCACATTGG CTACTCCATC CGTCCATCTG AAAGAGGCAA GGGTTATGCA | 360 |
| AAAGAACTCT CCGTCAGGGC TTGCAAGTTG CTAAGGAAAA GAACATCAAG AAAGCTCTGG | 420 |
| TGACCTGTAG CGTGAATAAT CCTGCTAGCA GAGCATCATT CTA | 463 |

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

| | |
|---|-----|
| CTCTTACGTG ACCAGAACAT GCTACTTCCC ATCCGAGAAG CCATTCTATC TGGCTTACCA | 60 |
| GTGTTTGGGA CCTGTGCGGG CTTAATTTTG CTGGCTAAGG AAATCACTTC TCACAAAGAG | 120 |
| AGTTATCTAG GAACTATGGA TATGGTGGTC GAGCGTAATG CTTATGGGCG CCAATTANGA | 180 |
| AGTTCNAC GGAAGCNNA TGTAAGGGAG TTGGCNAGAT TCCNATGACC TTTATCCGTG | 240 |
| GTCCGATTAT CAGTACTGTT GGTGAGGGTG TANAAATTCT AGCAACAGTG AACNATCAAT | 300 |
| TTGTTGCNNC CCAAGANNA AATATGTTGG TAAGTCCTTT TCATCCAGAA TTGACTGATN | 360 |
| ATNTGCGCTT GCNCCAGTAC TTTATCAGTA TGTGTAAAGA AAAAAGTNGA GATTGAATTT | 420 |
| CTCCAACTTT NCCACNTGTA ATNNNCAATN NCNATGTATT GGAGTACGGA CGCAG | 475 |

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

| | |
|---|-----|
| CCTTCAAAAA TTATTTGATG CAACCTTAGA CAATCCAGAA CTCACCGCAA CATTAGTGCC | 60 |
| TTTAGGAGAT GGTATTCTCA TGCTTCGTAA AAATGTAGCA GATGTTCAAC TGTCTGAAAG | 120 |
| CGAATGATTT TCAGAAAAAT TTAAGAAAAA ATAGTAAAT AGATAGAGTA ACACTTATCT | 180 |
| CAAAGGAGTA GACATGAAGA AAAATTATT GGCAGGTGCC ATCACACTAT TATCAGTAGC | 240 |
| AACTTTAGCA GCTTGTTTCA AAGGGTCAGA AGGAGCAGAC CTTATCAGCA TGAAAGGGGA | 300 |
| TGTCATCACA GAACATCAAT TTTATGAGCA AGTGAAAAAC AACCTTCAG CCCAGCNAGT | 360 |
| CTTGTTAAAT ATGACCATCC AAAAAGTTTT TGAAAAACA ATATGGCTCA GAGCTTGATG | 420 |
| ATAAAGAGGT TGATGATACT ATTGCCGAAG A | 451 |

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

| | |
|--|-----|
| CTATGGATAA GGCACCTTGCT GACCTCAAAA CATCAGGGCA CTTGCCTATT CCGCGACACC | 60 |
| TACGTGATGG GCACTACANT GGAAGCAAGG AACTGGGGAA TGCCCAAGAC TATCTCTATC | 120 |
| CACACAATA TCCTGNAAAT TGGGTCAAGC AAGACTATCT GCCACAAAAA ATTCGTAATC | 180 |
| ATCACTATTT CCAAGCAGAA TATACTGGTA AATATGAACG GGCTTTGGCT CAAAGAAAGG | 240 |
| AAGCTATCGA CCATTTCGA AAAATCTGAA ATCCTTTTCA AAAAATTGCA CTTTCCTCTT | 300 |
| GATTTTMTT GAAAAAGTGG TATCATATAA ATATAGAAAC GCTGTGGTGT ACGACTTCAC | 360 |
| ACTTAAGTGT TGACCGACTA TTTTGTAT TATTANGGAA ACAAAGTCT TCTGTCAGCA | 420 |
| TGTAGGCCGT CTCACACGGA AACAGCTTCA GTT | 453 |

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

| | |
|---|-----|
| CCGTAGTACA GGCACAAAAA GATTTGAAA ATAGAAAAAG AAAAGCCAAG AAAAAGGCTC | 60 |
| AGAAAACGAA ATAAATAAGG AGGAATCTGG TAATGGTAGT ATTTACAGGT TCAACTGTTG | 120 |
| AAGAAGCAAT CCAGAAAGGA TTGAAAGAAT TAGATATTCC AAGAATGAAG GTCATATCA | 180 |
| AAGTCATTTC TAGGGAGAAA AAAGGCTTTC TTGGTCTATT TGGTAAAAAA CCAGCCCAAG | 240 |
| TGGATATTGA AGCGATTAGT GAAACGACTG TTGTCAAAGC AAATCAACAG GTAGTAAAG | 300 |
| GCGTTCGAA AAAAATCAAT GATTGACG AGCCTGTGAA GACGGTAGT GTAAGAAACC | 360 |
| GTTGACCTTG GTCATGTGGT TGATGCTATT AAAAAATAG AGGAAGAAGG TCAAGGTATT | 420 |
| TCTGATGAAG TC | 432 |

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

| | |
|---|-----|
| AAAATCAAGA AATTCTTTGA AGGAACGACA GATACAGCTG AGAACTATAT CAAGTCGGCC | 60 |
| CTTAAAATGT TGGTCAAATA GGAGCAGAGA ATGACAAAAC GTTGTTCTGT GGTCAAGATG | 120 |
| ACCAACCCGC TCTACATCGC CTATCATGAT GAGGAGTGGG GTCAGCCCCT CCATGATGAC | 180 |
| CAAGCATTTG TTGAGTTGTT GTGTATGGAA ACCTATCAGG CAGGCCTGTC TTGGGAAACG | 240 |
| GTACTCAACA AACGCCAAGC TTTCCGAGAA GCCTTTCCAT AGCTATCAAA TTCACTCCAG | 300 |
| TCGCAGAGAT GACTGACACT GAATTGGAAG CCATGCCTGG AGAATCCCAG CTATCATTC | 360 |
| GAAATAGAGC CCAAGATTTT TGCTACACGC CGCCTAACGC CCCAACCCTT TCCTACAGTT | 420 |
| ACAGGCAG | 428 |

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

| | |
|---|-----|
| CTATTAGATG GTATTGACTG CCCAGACACT TACGGATCTA GCTGAGACAG GGAATTGTCC | 60 |
| ATAACCTTCC TCATCAATTG TAACTTGACC TTGGTGGTTA CCAAGTAAAT CTACAAAGGT | 120 |
| TTGATTAGTC CATTCTTGAC CGACAAACAT TGACTTGCTG TTTTCTTGGT CATTTGAAAT | 180 |
| CAAGACTGCG ATTGGGGATT GATTTTCAGC ACCTGAACGT ACCCAACCGA TACAGTTAGC | 240 |
| ATGGTCAAAG TAGTCATTTT GTTCTCCATA GGCCAAATCT TTTCGGATGG CTAGGAGGCG | 300 |
| GTCAAGGATT TCTTTGAAAT CTTGTTGAGC ATACTGGCCT GAAATCCCAT AGTAGTCTCC | 360 |
| GTAAAAGACA CATGGAAGGC CGTCTTGGCG TAACAAAATG AGGGCATAGG CTGCTGGCTT | 420 |
| GAACCATTCT TCAACGGTAG ACTCAAGGGC TTGTCCTCGT TGGGTATCGT GGTTGTCGAC | 480 |
| AAAATCACAG ACTTGTCAGG CTTGAGTTCA ACCAGGCT | 518 |

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

| | |
|---|-----|
| CTCTGTCCTT TTACCTGAGA GTTTGAGCAG TTGCCTGCCT TGCCCCCTCG GTGCCTTTAC | 60 |
| GGTCTCTCCA GAGTTCCGTC CATTTACAGT CATGGAAAAT CAAACGATTC CCCACTTCTA | 120 |
| TTAAACTTCA TTCGGTGTG GTATTTAATT GATTCTAATT TTACAAAAA TGTTGGCTTT | 180 |
| TGTCAATGTG TTTATTAGTA AAAATTAGTT CAACAGTTTT TACTTTATAA AGTCCAGAAT | 240 |
| ACTGCTATCC TTTAAAAGTG ACAATAGTCG CACCACTGCC TCCAGCATTT TGTGGGGCAT | 300 |
| AGCCGAAACT CTTGACATGT TTGTTTCTTT GCAAGTATTT GGTAACCTCT TCACGGATGA | 360 |
| CTCCTGTTCC GATACCATGG ATGATATCAA CTTGAGCCAT ATTGTTAAGC AAGGCTTGGT | 420 |
| CGAATGAAGG TATCTAGCTC ATTCATGGCT TCTTCATAGC GCTTGCCTCG AAGATTCAGT | 480 |
| CTAGCTTGAG TCCTCGCCCA GAAGTTCC | 508 |

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

| | |
|--|-----|
| CTCTTGGGCT CTCTTCTCAG CAACTTCCCT GCTTTCACCT TTGGTCTTGA TAGGTGANAA | 60 |
| CGTAATATNT CCAATCMNNG TCATATTAGG AAANAGTTAA ATTGTGGAA AACCATGCCC | 120 |
| ATCTTCTCAC GCATGGGAAA CAGGTCATTC TTCTTGTCGG TAATATCGAC TCCCTCAAAG | 180 |
| ATAACCTTCC CCTTGGTTGC TTCCTCCAAC AAATTCATAT AGCGAAGCAA GGTAGATTTC | 240 |
| CCACTCCCTG AAGGACCGAT GATAACGACA ACTTCTCCTC TTTTAATCTC GAGGTTGATG | 300 |
| CCCTTCAATA CTTCAATTCTT TCCAAAAGAT TTATGTAATT TTCAATTTTT ATCAAGGTTT | 360 |
| CTGTCATTAT TTCTTATC | 378 |

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION. SEQ ID NO:209:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGGCCAGCC | AGATAAACCT | CGATACGGCT | TTCTGCTCGT | TTGATGCGTT | GCAAGAGTCC | 60 |
| GCCCATACGG | ACGTCAACTG | TATCCAAACC | AAAGACCTTG | TTTTATTTCA | GCCAGTGGTG | 120 |
| ACTAAAGAGG | GCATGGAAGT | CTTCAATTTG | GCTTCTAAGT | TCTGGTAATT | CTTGTCTGGC | 180 |
| GATTTGTTGT | AAACTTTCTT | TATCATCCGC | TTGGTAGGCA | TGACGAATGC | GTCGTCCAC | 240 |
| ATCTACTTTG | CTACTTAAAA | TAGCATTCAA | CTGGGCCTGA | GTTTCAAAGA | GATAAGCATA | 300 |
| GTTTCCAGCT | TTTTCTTTAA | TGTCAGCAAT | AGTTCCCGCC | GCCTGAGCGA | AGTGTGGCTT | 360 |
| GTCCTGTTCA | GGTGTCTATG | GTCGGTCAAG | TATCGGACAG | AGAACATCCT | GATAAAAGAC | 420 |
| ATAGCGGTTG | GGATTGATGC | CACTGAGATT | ACCTGGTAGG | TCTGGTAAGA | GGTTGGCAAG | 480 |
| ATCAATCTGC | ATAAAATCCT | CAACCGTTAG | ACCAGTATTG | GTCTTGAAAT | GCGCAGACAA | 540 |
| ACTATCTAGG | TCATTGCGAT | AGATCAAGTT | ATCGATACCG | TCGACCTCGA | GGGGGGCCGT | 600 |
| ACCCAGATTT | GCAAGCTTGG | TAGGATAAAG | AACTGGGCAG | TTTCACCACC | ATTGTCTCCC | 660 |
| CAACCCGTTA | CGATGACTTC | TTTAATCTGA | TTGGCACGGC | AGGCTTTATT | AGCCTCGATA | 720 |
| GCCACTAGAC | GGCTAAATG | G | | | | 741 |

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|------|
| AAACTCGATT | TGAGAGAAAG | TCCAATAAGT | CTTTCCATAA | TAAAACGCAT | AGTAGCAAGA | 60 |
| GTTTCTACAC | CCACTATTAT | GCGTTTTTAT | CATTTTGAAA | TCTACTGCTA | ATCAATGAAG | 120 |
| AAGCAAAGAT | CAACTAGGC | AGCTAGTTAC | AAGTTACGTA | AGCGCCTCAT | AACAAGGTAT | 180 |
| CTATCCTAAT | TCCCAACTT | CCAGTATACT | AGATAAAAAA | TAATTATCGG | AGGAAAGGTA | 240 |
| TTGTACTATG | ATAATTCAAC | TAAGTGATTT | AGGTCAAGTT | CACCTTGTTT | GTGGCAAGAC | 300 |
| AGATATGAGG | CAGGGAATAG | ACTCATTAGC | CTATGTAGTT | AAAACCCACT | TTGAATTGGA | 360 |
| TCCTTCTCC | GGTCAAGCCT | TTCTCTTTTG | TGGTGGACGT | AAAGACCGCT | TTAAAGCCCT | 420 |
| TTACTGGGAT | GGTCAAGGAT | TTTGGCTACT | ATATAAACGC | TTTGAGAACG | GAAAACCTGAC | 480 |
| TTGACCAAGT | ACAGAAAAGG | ATGTCAAAGC | TCTCACACCA | GAACAAGTAG | ACTGGCTTAT | 540 |
| GAAGGGCTTT | TCTATCACTC | CCCAAATATA | GTGGATTTAA | ACTAGAATAG | TACACCCCTA | 600 |
| CTTCTAAAC | ATTGTTAGAA | ATCGATTTGA | CTGTCCTGAT | CAATTTGTCC | TGTTCTTATT | 660 |
| TCATTTTACT | ATAGAATCCA | TCTGAAAGCC | GTTTATGATT | TCTATTGAAA | TGAAGACCGT | 720 |
| CCATTTTAGT | AGACTAAAGG | ATTACTCAAA | ACTTCGAGAA | GGAAGACAGA | TGAACCTGTT | 780 |
| TCTTATAAAA | ATGTTGTCTG | AAACTATTCTG | CTTTTTTCCA | GAAATTTTAG | AGGAAGAAAA | 840 |
| CTTTATGAGG | AAAAAGGAGT | TACTCAAATA | ACAATTCAGG | ATTAAAAATA | GACAGTTGAG | 900 |
| GAGCGGAAGG | TATAAATTAA | GTTTGCTACT | GTATAATGGA | TTTAAATCAC | TCAGCAGACA | 960 |
| GAACGAATAC | TCTTCGAAAA | TCTCTTCAAA | CCACGTCAGC | TTGCGCTTGC | CGTAGATCCA | 1020 |

| | |
|---|------|
| TAGGGGACTG GACTTCATCA GTTCTATCAA CAACCTCAAA ACAGTGTTC GAGCTGACTT | 1080 |
| CGATCAATTT TATCTGCACC TCAAAGCTGT ACTTTGAGCA AGCCTGACGA CTAGCTTCCT | 1140 |
| ATTTGATTTT CATTGAATAT CAGAACTCA TTCTCCATCA AATAATTCGA CTGCGTCTAA | 1200 |
| TAATTTTGG TCTGGCACGG TGTCAGAAAT AAAGGTGTG TATTGGAGA GGGGATTAAT | 1260 |
| TTTAAAAAAT CCAGTCTTGT AAAATTTAGA ACTATCAATC AGTAAGATGG TTTCATGGGC | 1320 |
| TTTGTCAATA ATATTCTTTT TTGAAATAG | 1349 |

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

| | |
|---|------|
| CTTTTTTATA AGCAATTCAA TTTTATACTC ATCTGCTTTC AAAAAGCATT CTAGTCCATC | 60 |
| TCCGATTAAC GATGGACTTT ATCACCTCCT TCTCCAATCC TTGTATGACA TCTTGAAGTT | 120 |
| GATTCATGAC ATCTTCCAAA ATTCGAAAGG CTTTATTCTT AAATCCACGT TTACGAATCT | 180 |
| CTTTCCACAC TTGTTCAATG GGGTTCATCT CTGGTGTGTA TGGAGGAATA AATGCAAAAC | 240 |
| CAATATTAGT CGGAATCTTT AAGACACTTG ATTTATGCCA TATAGCATTG TCCATAACGA | 300 |
| GTAAAAAATA ATCATCTGGA TAAGCTTGTG AAAGCTCTTC TAAAAAGGCG TTCATCCACT | 360 |
| CAGTATTACA TCTACCAGCT ATTAAGAAAA AATGATTCCG CCTGTTATGG GCATCAACAG | 420 |
| CTCCATAACA ATAGTGAAAT TCTCGTATAT AGTGAATATG GACATGTGGA CCTACTCCTA | 480 |
| TTGGAGACCA ACAAGATCCC AGTTTACTGA TTCTACCGAA ACCAGCCTCA TCTTGGTACA | 540 |
| TCAAGCGAAC CTTATGAAAA CGTCTACTGG TTTAAATCGC TTTCTTGTCT TCTTGAATTG | 600 |
| AGATTTTATT TTTAGACGCG ACAATGGTTT GAGCGTCTGC TTTCTTAGGA TGTTCTGGAC | 660 |
| GTGGCATAAT ATTCGCCAG CCATGGCGCT TCAACAGTTG ATAGAAGGCA TCACGTGTGT | 720 |
| AGGAACGACC TAACTCCTTT TTATAAGCCT GAAATAAGGC ATCAATTGTA ACAAATTCTC | 780 |
| CTGCCTCTGT AGCCTTCAAA TGGCGGGCAA GAAATACTTT CTCTTCCTCA ACTGTCATAT | 840 |
| ATGCATGGTT ACACCACCAC TTTCCTGATA GAGTTGTTCA CATCTTATTT CAAACTACTA | 900 |
| TAAAAGTTCT ATAATCTCTT TATAAGATT GCCCATCAGA CGAAATATAA TAAATTGAAA | 960 |
| CTAGAATAGT ACACCTCTAC TTCTAAAACA TTGTTAGAAA TCGATTGAC TGTCTGATC | 1020 |
| GATTTGCCCT ATTCTTGTTT CGTTTACTA TAGAACGATT TGAAGGCGTT TATGATATTG | 1080 |
| AGCTGTACGA GAGTCTTTTA AAAGTGTTTT GATGGCTTGG ATTTCTTCTT TAGTTGATTT | 1140 |
| CATATCACTA TTATATAATG CTTTTTGATC TTTAGTTTAG TATTATCGTA GAAAATGGAC | 1200 |
| TAGGTGCTAT GGATACACCG GATGAGAATG GTTATGTAGC AGATGACTAT CGGATTACTT | 1260 |
| ACTTAGAGGC CCACATCAAG GCCATGCGAG ATGCCATTTA CCNAGACGGG GTTGACTTGC | 1320 |
| TTGGTTATAC GACTTGGGGC TGTATCGATC CAGTTTCAG | 1359 |

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```

CTAGTATTTTC CGTTGTGNTT AGTTTGTCTG CCTATGGAGT TATTGCCTAT GTGCAAGGTC      60
AGNTGGATAT TCTTCTAGTG ATTCTGGCCA TGATTGGTGG TTTGCTCAGT TTCTTCATCT      120
TTAACCATAA GCCTGCTAAG ATCTTTATGG GTGATGTGGG AAGTTTGGCT TTAGGTGGAA      180
TGCTGGCAGC TATCTCTATG GCTCTCCACC AAGAATGGAC TCTCTTGATT ATCGGAATTG      240
TGTATGTTTT TGAAACAACT TCTGTTATGA TGCAAGTCAG TTATTTCAA CTGACAGGTG      300
GTAAACGTAT TTTCCGTATG ACGCCTGTAC ATCACCATTG TGAGCTTGGG GGATTGTCTG      360
GTAAAGGAAA TCCTTGGAGC GAGTGGGAAGG TTGACTTCTT CTTTGGGGGA GTTGGGCTTC      420
TAGCAAGTCT CCTGACCCTA GCAATTTTAT ATTTGATGTA AGAATGGCAC CCTGATGTTT      480
TAGGGTGTTT TTGTGTTTAA ATACACAATG AAAATCAAAG AACAACTAG AAAGCTAACT      540
TTAGGCTGCT CAAAACATAG TATATTGAAA CTAAAATAGT ACACCTCTAC TTCTAAACA      600
TTGTTAGAAA TCGATTTGAC TGTCTGATT ACGATTTATC CTGTTCTTAT TTCATTTTAC      660
TATACCATCA ATAAGTGTG AAAAGATCGT TGACAGAACT GACCAAGCCA GATCATCTTT      720
GTAACCACCT TGAGCTTGTA GCATATTTGT TAATTGAGCA AAGGCGCTAG AAGAGTTTGC      780
TGGGTCAGCA GTTGGCATT TCCCTTTTAG TTCAGGTTTG AGAAGGTCGC TATATCCTTC      840
GATGTTTCATG CCTTTAGTTA AATCAGGGTG GACGATTAAA ACACTACCAT CTAGTGATA      900
AGGAGTAGAG AAGCCAGTTG TGTTTTGATA TTCTTTGATA ACATTATCAT TTTCTTTTGA      960
AATATAGTTT TCAAAGAGTT CTCCTGGGGT AGCATATTGT GTTATAAGAA CCACCAAAGA      1020
TAACATCAGC TACAGGAACT TCTTTTCTG ACCTAGTTTT TTGAAAAGTT CTCCAGTACC      1080
AG                                                                                   1082

```

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```

CTGGACTTGA TAGGCATCTT TGTAATCCTC TAAAGCCTCT TTCATCAAGG CACTACCAAT      60

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| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| TCCTTGACGC | TGATAGATTG | GTAAAACGAT | TAAATCCTGA | ACCAATACTG | ATGAGAATCC | 120 |
| ATCTCCAACC | AAACGAATCA | AGCCCACCAC | AGCATCACCA | TCAAGTGCCA | CATAAATTAC | 180 |
| TAATGAATGA | GATAAGGCCT | GCTCCAGCAT | CTCTGGTTGA | TGGGTATAAT | TAGTCCAACC | 240 |
| GACAGCCTGA | TAGACATGTA | AAACATCCTC | TAGCTTGACA | ATTTCTTGCT | TTTAAATAGT | 300 |
| AATCATCTCA | ACACCTCTTA | AAGTTCTCTC | AAGCTCTTGT | ACTGCTGTCC | ATTTTATCA | 360 |
| AAATTTTCAG | GACGCAACCA | TGTTTCCAAA | CGATCTTTGA | CTTTGGGCCA | GTCCTTATCA | 420 |
| ATCATAGACA | ACCAATCCAT | ATCTCTCGTA | CGCCCCCTAT | AAACCACTGC | CTGACGGAAG | 480 |
| GTTCTTCAT | AAATAAGCC | CAAACGCTCC | GCAGCACGTC | TGGATGGCAG | GTTAAGAGCA | 540 |
| TCGCATTTC | ACTCATAACG | ACGATAGTTA | AGCTCTTCAA | AGACATAGCG | AGCCAGTAGA | 600 |
| TACTGGGCTT | CTGTCCCTAT | CCGTGTCCCC | CTGAGTTTGT | GAGAAAAAGT | GACAGCTCCC | 660 |
| ACTTCTATTA | CTCCGTTACT | GGTCAATACG | CATGAGAGAA | AAATTCCCAA | AGCCTTACCA | 720 |
| GTTGCCTTGT | CTATGTAGTA | AAAACGGTCC | TTACGAGCCA | ACATCTGACT | ACTATAGTAG | 780 |
| ATTGAACTA | GAATAATATA | CCTCTACTTC | TAAATATTG | TTAGAAATCG | ATTTGACTTC | 840 |
| CCTGATCGAT | TCGTCCTATT | CTTATTTTCT | TTTAATATAA | TTGATAGTGG | TCGCCCCAGC | 900 |
| CAGATACCTT | ATCTGCTATC | CATTTAGGAA | CCCTAACTT | AAGCAATCCC | CATAATCGTC | 960 |
| TCGATTTCTT | CTTCCATTGC | TTCCAGATAA | TCACTCGTAG | GCGAGTACGC | AAGCGCTCAT | 1020 |
| CTATGTTAGT | GACTATACTT | TTCATATTTA | TAATTCATT | CTTTCGTTTC | ACTCAAGGCA | 1080 |
| CAACACAGAA | TGAAAAAGTG | TTGTGATCTT | TATTTTGTTC | TATAATAATA | GTGAGAAAGC | 1140 |
| CTATCACTAC | TACAAATCAC | GGGGAGGTGA | ATAAGTGAGT | GGTACAGCCA | CTACCTCGCA | 1200 |
| TATTTTGTCA | CATCATTTAA | CGGTACATAA | TAAGTTGTAC | CATCTGAATA | AGTTGCTACA | 1260 |
| ATATCATTTG | CATGCTCTCC | TTCACCTTTA | GCAAAGGTTG | GAG | | 1303 |

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| CTCTTCAATC | AACTCACGCT | TTAGGGCTTC | CTGATGATTT | TCACCTGCTT | CAATTTCTCC | 60 |
| ACATGGTAGG | AACCAAGCAC | CATTTGGTTC | TTGAACAAGA | ACAATTTGTT | TTTGTTTCAGG | 120 |
| ATTAGGGATA | ACTGCATATA | CGCCATAGCG | AGCAATATAG | TCTGTATTTC | CTTTTCTCTC | 180 |
| CGAAAGTTGG | GTTTGCCATT | GCATTTTCCT | CATTATCTAG | TATCGTTATT | ATTATAGTGA | 240 |
| AATGAACCAA | AAATAGTACA | CAATGTGGTA | TAATCTTTTT | ATGGCATATT | CAATAGATTT | 300 |
| TCGTAAAAAA | GTTCTCTCTT | ATTGTGAGCG | AACAGGTAGT | ATAACAGAAG | CATCACACGT | 360 |
| TTTCCAAATC | TCACGTAATA | CCATTTATGG | CTGGTTAAAG | CTAAAAGAGA | AAACAGGAGA | 420 |
| GCTAAACCAC | CAAGTAAAAG | GAACAAAACC | AAGAAAAGTT | GATAGAGATA | GACTTAAAAA | 480 |
| CTATCTTACT | GACAATCCAG | ACGCTTATTT | GACTGAAATA | GCTTCTGAAT | TTGGCTGTCA | 540 |
| TCCAACCTACC | ATCCACTATG | CACTCAAAGC | TATGGGCTAC | ACTCGAAAAA | AAGAACCACA | 600 |

WO 97/37026

PCT/US97/05306

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| CCTACTATGA | ACAAGACCCA | GAAAAAGTAG | CCTTATTTCT | TAAGAATTTT | ANTAGTTTAA | 660 |
| AGCACCTAGC | ACAGGTCTAA | CAAATGGTGA | ATTAATCGCT | CCAATGACTT | ACGAAGAGAT | 720 |
| GATGACGAGC | GACTTTTTTG | AAGTATGGTT | TCAGAAGTTT | CTCTTACCAA | CATTAACCAC | 780 |
| ACCATCGGTT | ATTATAGTGA | AATGAAATAA | GAACAGGACN | AATCGATCAG | GACAGTAAAA | 840 |
| TCGAATTCTA | ACAATGTTTT | AGAAGTAGAG | GTGTACTATT | CTAGTTTCAA | TCTACTATAT | 900 |
| TAATGGACAA | TGCAAGATTC | CATAGAATGG | GTAAGCTAGA | GTTCTTATGT | GAAGACTTTG | 960 |
| GGCATAAACT | TTTACCTTTT | CCTCCCTACT | CATCTTAGTA | TAGAAAAGTG | AATCTAAAAAT | 1020 |
| AGTACATAAC | TGCTTCTAAA | ACATTCTTAT | AAATTGATTT | AAATTCTCAA | ATCATATTAT | 1080 |
| TCAGTTCTTA | TTTCATTTTG | CTCTACAATC | CTGTTGAGAA | GACACGTGTT | CATATCAAAA | 1140 |
| AGGTATTGGC | AAGTTGCAAT | ACCTTTTTAC | AAGGTTCTTT | TGTCTTATTT | TTGTTTCAAC | 1200 |
| TGACTATATC | TCCTATGGTT | CTAGTTCAGA | AGGCTAGGCT | ATAATTATGA | TTGATAAGAA | 1260 |
| GTATCATTCC | AAGTATTGAG | AGTGAATGTT | TCAAAATCAT | GGGTTTCTAT | AATGGTCAGG | 1320 |
| CTGGCATTTG | CTAGACCGCC | ATCTTTACGA | AGAAGTGGTT | CTTTATAGCC | TAGGAGAGTA | 1380 |
| CGAAGACTGG | CAGTAAGATT | GGCGCCGTGT | CCGACAATTA | GAATACGCTC | AGCTGGACTA | 1440 |
| TCTTTTAATG | ATTTGATAAA | TTGGATGGTC | CGCTGAGTTG | TACTATAGAG | GGATTCCGGCT | 1500 |
| CCGAACATTC | GAGTGTCAAA | TTGAGCAAGA | TTTGAACGAA | AAGCCTGGAT | TTGTTGCGGG | 1560 |
| TAAATAG | | | | | | 1567 |

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGTTTCCAT | AGCATGACTT | CTGTACTAGA | CTTCTTTTTC | CGAATAAATA | GATAGAACCA | 60 |
| CAGAATCTAG | TAAACCTAGA | ATTAAAATTA | TGGTATAATA | TTAGCAATAA | AAGAAATCTG | 120 |
| GAGGATTAGA | ATCATGGTAT | CAACGAAAAC | ACAAATTGCT | GGTTTTGAGT | TTGACAATTG | 180 |
| CTTGATGAAT | GCAGCAGGTG | TGGCTTGTAT | GACGATAGAG | GAGTTAGAAG | AGGTCAAAAA | 240 |
| CTCAGCGGCA | GGAACCTTTG | TTACTAAGAC | AGCGACCTTG | GACTTCCGTC | AGGGGAATCC | 300 |
| TGAGCCACGC | TACCAAGATG | TTCCACTTGG | TTCCATCAAC | TCTATGGGCT | TGCCAAATAA | 360 |
| TGGCTTAGAC | TATTATTTGG | ATTATCTTTT | AGATTTCGAG | GAAAAAGAGT | CGAACCGAAC | 420 |
| TTTCTTCTTA | TCTCTGGTCG | GCATGTCTCC | AGAGAAACCC | ATACTATTTT | GAAAAAAGTC | 480 |
| CAGAGA | | | | | | 486 |

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

| | |
|--|-----|
| CTCTATCAGG AAAGTTAAAT TAATTTATAG AAATATTTTA GTATTTAAGC CCTACTGTTA | 60 |
| TAGATTCAAT ACACTATATA TGTGTTTGTC TGATAAAAT TTCTACTCTT TTTGATTTTA | 120 |
| AATAAGTATT AGTTTACATT ATGGTGTGAA TTGGGTTTGA TATCTCTTTT GAGGAAGTTG | 180 |
| CCTTAGATTT TTCTGATTGT GTTTTATTGT ACAGTGTATC TTGCTTGTTT TGAACAGAAT | 240 |
| TTTTTATGAC ATTTGTCATA TTTTCTAGTG ACAGAAGCTT CTGCCTCCTC TGATTTTAAA | 300 |
| AGACTATAAT TGTAAGTATGA AATGGGGGAA GAAGAGATGA GAAATAAAAT GATTATCGCA | 360 |
| GTAAGTTTAG TAGTAGCAGG AGTTATGACC TATCTCATGT TTTCTGGGATT GGATGAGAAT | 420 |
| TTCTACCATT TTCCTTGGA GGTCTTTGCT GGCTTTGGAA TCATCTTCTT GGCTTGTCCTA | 480 |
| GAGAAGGTTT GAAATTAGTA AGAGATGTGA AAAAGGAGTT TGAAAAATGA AAAAAGCAAC | 540 |
| TATCTATTTT TTTATCGGCC TGTCACCTCTT GGTATGGTTG GTAGAAATGT TTACAGGTTG | 600 |
| GTTTGCTCAA ACCTTCCTTC ACCAGTTCAT CCGTGGTGCA TGGGGATTAG GATTTATGAT | 660 |
| TTTTATCGCC TTTCCGATGG GAAAGGAGTT GCTGGAAGGA GAATATCATG AACATGATTA | 720 |
| AGGTTCAAGG ACTACATAAA AATATTAAGG GCAAGGCTAT TTCAAAGGAT ATTCCTTTG | 780 |
| AAGTAGCAGA AGGTGAATGC GTTGCCTTGA TTGG | 814 |

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

| | |
|---|-----|
| CTTGGTACGA CCGTATGGGT GGTCACGTGA AGTGGGAAAC TTCCAAGATG GGCACGTGTG | 60 |
| ACGGATCCCC GTAAACTGTC GCANAAGAAC TGAAGATGAT GTTTTACAG TTGTTTCTT | 120 |
| CCATGGCTTT CAAAAGGCTG ACAGTTCCAG CGATATTGTT GTCATAGTAG GCAAGAGGGA | 180 |
| TACGTGTTGA TTCGCCAACA GCCTTCAAAC CAGCAAAGTG AATGACACCA GTCAGTTCTT | 240 |
| CCTGCTTGAA AATATCTCTG AGGGTATCTG TGTCACNAAT ATCTGCCTCA TAGAAAGGAA | 300 |
| TCTCAACTCC TGTGATTCTT TCAACAACCT CTAAACTCTT ACNATTGCTA TTGACAAGAT | 360 |
| TATCCACCAC AACAACTTGA TGGCCTGCTT GGATCAATTC AATAACAGTG TGGGTTCGAA | 420 |
| TAAAACGGGC ACCACCAGTT ACCAAAATCT TTTCTTGCAT CTTTTTCTT CGATTCTCAG | 480 |
| ATTATTTTTT CTTATTTTAA CCATTTTGA CAGGGAATGT CATTTGCCAC CTAAACTAC | 540 |

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|------|
| CTGATAAAAT | TTCAGTAAAA | TGCTTATACT | CTTGGAATAAT | CCAATTCAAA | CCACGTCAAC | 600 |
| GTCGCCCTGC | CATGGGTATG | GTTACTGACT | TCGTCAAGTTC | TATCCACAAC | CTCAAAGCAG | 660 |
| CGCTTTGAGT | AACCCGCGGC | TAGTTTCNTA | GTTTGTTCTT | TGATTTTCAT | TGAGTATTAT | 720 |
| TCGCTTTTAA | CTCGTTTGAC | ATAGTTTTC | ATTGGGTAGT | TTTCAGGGTC | CAAGGTCAAC | 780 |
| TCCTTGCTCT | GGATCAGTTG | AGCTAAATGG | TAACCAATAA | TAGGACCAGT | TGTGAGGCCT | 840 |
| GATGAACCTA | GTCCACTGGC | TGCATAGACA | CCAGTTAAGT | CAGGCACCTG | CCCAAAGAAA | 900 |
| GGAGAGAAAT | CACTGGTGTA | GGCACGGATT | CCAACACGCT | CAGATTTTGA | AGTAGCTTCA | 960 |
| GCCAAATCA | GATAGTGAGT | CAAGGTGGCC | TCCTCCATTT | GTTGGAGCAA | GGTTTCATCT | 1020 |
| ACCGTCAAA | CAAATCCCAT | GTCATTTTCG | TGGGTAGCGC | CTAAGGACAA | TTTCCCACCT | 1080 |
| GCAAAGGAA | TCAAATCCCA | CTCCCCTTCT | GGCATGACAA | CAGGGTAAGC | TTCCATGTCT | 1140 |
| TGGACCAGCT | GATAATCTCG | TAGTTGTCCT | TTTTGAGGAC | GAACATCTAC | TTCATAACCC | 1200 |
| AAGGGTTCTA | ACATGTCCCC | CAACCAAGCT | CCNGTCGCCA | AAATAACCTG | CTCAAATCCC | 1260 |
| TCTTCACCAA | TCTGGTAGCC | TGATGCTAAC | GGTGTGAGAG | TCACTTTTTC | TTTGACCAG | 1319 |

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CTCAAAATAC | TGTTTTGAGG | TTGCAGATGG | AAGCTGACGC | GGTTTAAAGA | GATTTTCGAA | 60 |
| GAGTATAAAC | TGCTTATAAA | ATAAAAAGGA | GCCCTGATGG | AACACATTAT | TTATCAGTTT | 120 |
| GAAGAGGACT | TGGCAATCCT | TACCTTGAAC | CGTCCTGAGG | TCGCAAATGG | TTTTTCATATT | 180 |
| CCCATGTGTG | AGGAGATTTT | AGAAGCTCTG | ACTTTGGCAG | AAGAAAATCC | AGCTGTGCAT | 240 |
| TTTATCTTAA | TCAATGCCAA | TGGAAAGGTC | TTCTCAGTTG | GGGGAGATTT | GGTAGAGATG | 300 |
| AAGCGGGCAG | TGGATGAGGA | TGATATTCCA | TCATTGACAA | AAATCGCAGA | GTTGGTCAAT | 360 |
| ACGATTTCTT | ATAAAATCAA | GCAAATAGCC | AAACCTGTTT | TTAATGGAAG | TTGACGGTGC | 420 |
| TGTTGCAGGT | GCCGCAGCGA | ATATGGCTGT | TGCGGCAGAT | TTCTGTTTGG | CGACGGATAA | 480 |
| GGCTAAGTTT | ATCCCAAGCC | CTTTGTTGGT | GTGGTTGGCT | CCAGATTCCA | GGGG | 534 |

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

```

CTGCAGCCGG AAGTTATCTG GTTACAAAAA ATCGCCAAAC CATCACAGAT GAAAGTCTTG      60
AATACCACTG ACCGCGTTCA AGCTATCAAG GACGATGTGG ATATTATCCA AAACAGCCTG      120
CAAATCATTA ACCAGCAAAA AGAACTTATC AAGGAATACC AAGAAGACTT GACTTACAAG      180
TTTAAGGTCT TGGAAAAGGA TATCCAAACT AGGACTAGCT GTGATAAAAG AAATGCAGGG      240
AACTGAAGAT AAGTAAAAAG AGCCCGACGG CTCTTTTTTA AAACGTAAAC AAGTTATAGT      300
GAATTGAATT TAGAATAGCA CATCATAGTT TCTAAAGCAT TGTTAGAGAT TACTTTAAAA      360
TCCTCTTATC AATTTGTTC TATTCTATTT CAATCTACTA TATATATCCC ATCAACTATG      420
CATCATAATT TAGGTAATC ATACTCAATA AAAATCAAAA AGCAAACTAG AAAGCTAGGC      480
ACAGACTGCT CAAAACACCG TTTTAAGGTT GTGGATAGAA CTGACGAAGT CAGTAACCAT      540
ACCCATGACA AGCCGACGCT GACGTGGTTT GAAGAAATTT TTGAAGAGTA TCATTACCA      600
TTTCACAAC AAATCGAAGA CTTTCTGCCG TAATGAAAAC ACCTGAAACA GCTTGGTTTC      660
AGCTGTCCGG AAACTTTAAG ACTTAGGTTT AAAGTTTAGG TATGGAACCT CGAAGGAGGT      720
CGCTACCGTC CGTCATTACT TAGNGAAGNC TTAAAAATC TATAAAGTAA AAAGAGCCCC      780
ACAG

```

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```

CTACTCGTTT TAGTATAGTA AACTGAATCT AGACTAGCAC AATGCNGCTT CTANAGCGTT      60
TCGAAACTAG AATAGSACAA CATAACTGCT AAAAGATTTT TATAAATTCA TTTGATTTTC      120
CTAATCAATT TGTCGTATC CTANTTCACT CCACTATAAA ATATTCTTAT CAATTGATTT      180
GNATGCCAAA ATTCCATCGT TCAGGTCTTA TTTTCATTNGG CTNTAAAAAA CTCTCCTGGG      240
NAATCCCAGG AGAGNATGAT TACNTATTTG AACTTGAATC CTTCTGTANAT AAGCTCTGTT      300
TTTGGAATTT GTTCTTAAT CTGTTTGGCA AGTGCCCTCA TCATAGAAAT AGGACCACAC      360
ATATAGACGG TTGCATGTTT GGGCACTTTT TTTGTTCAAA ATTAAGATAG CCGTCTTTTCG      420
TACTGTGAT TAGATGGAGT TCAAAATTAG GATTTTCTTG AGCATAGTTA CGGAGTAAAT      480
CTAGGTAGAC TGCATTTTCA TCTCCACGGA AGCTATAGTA GAAGTGAACC TGTTTATCTA      540
AAATAGGATG TTCACGGATG TAAGAGATGA AGGGGTGAT CCCAATACCT CCAGCAATCC      600
AAACCTGATT TTCTCGTCCT TCTTCTATGA TCATGTGTCC GTAAGCTCTG TCTAGGGTTA      660
CTTGCTGCC GCCTGAAGA TTATCATAGA TATTCTTGG TATGCTGCC TGAATTTTA      720
ACAGTAAAGT TAAAGAGTTT GAACCATGA ACTCCCTGAG AATAGAAAAG GGATGCCGGA      780

```

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACCACTTTCA | AAGCCTTCTT | GGAAAATCTT | TAGAAAGGCA | AATTGTCCTG | ATTGATAGTT | 840 |
| GAAAGGTCTG | CTAAGATGGA | TTTGAATTC | TCTAGTATCG | TGATTTAAGC | GTTTGAGATG | 900 |
| GGTAATTTTC | CCTAGATAGG | GGAAGGAAAT | CTTTTGATAT | AGAAAAATGA | TATAAAAACC | 960 |
| AG | | | | | | 962 |

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

| | | | | | | |
|------------|------------|-------------|-------------|-------------|------------|-----|
| CTCTTTCCAC | TATTATAACA | CGAAAGAAAG | AATTGTCAGG | GAAGTGTACA | GATTTCTTTT | 60 |
| CTATCTATTT | ATAACTCAAT | GAAAATCAAA | GAGCAAAC TA | GGAACTAGC | CGCAGGCTGT | 120 |
| AATTGAGTAC | GGCAAGGCGA | CGTTGACGCG | ATTTGAATTT | GATTTTCGCA | GAGTATTATT | 180 |
| CGTAAAAAAT | CTCAAAAAGC | CTACCTTTTCG | G TAGACTTAG | TTTGTTTCTA | TTCTAATCGG | 240 |
| CACTCTTCCA | AAATTTTGCT | CTGCTATACT | TGGCTTTCCT | AGTTGGTAAA | TCTGGTCAAC | 300 |
| CTTTTGAGTC | ATAGCATCCC | AAGGTTCTTT | GCCAATTCGG | CTGACTAGAT | TGACCTGTCC | 360 |
| TTTCAGAGAC | TTGAGATGTT | GCCTGCCTTT | TTCAGTAAAT | CCAAGGACAT | GAATGGCTTC | 420 |
| TGGCAAGTCA | CTTCTCTAG | CCTGCATCAA | AATATAGGTC | AATAGGCGTC | TGACACGCGC | 480 |
| CTTGGTGTA | CGTTTGGTAG | TCACTAACTC | GACCAATTCT | TCCACAGACT | GGGCTGTTTT | 540 |
| AATAGCTTCT | TTAATCGCGA | CAGCCATTTT | TTGATTGACC | TGATAGATGG | TGGTTAGGTC | 600 |
| GGGATTTGAC | AAGATTTGAT | AGCGGAGCAA | GGGAAAATAG | TCTTCCCAGA | TCACCTTACT | 660 |
| GGCTTGCTCA | AATAGGGCAA | CAGAAGGCAT | AAAACGTTCT | AAGAAATCTT | GGTCCTTCTG | 720 |
| ATGTTGACCG | AGGGCTGTCT | CCGAGGCAAA | GTCCACATCT | TTATTACACAG | AATGGTAACC | 780 |
| TGCCCCCTGA | CGCTGAATCG | GATGCAGCTT | GATATTCCGT | CCTGCAACCG | CCTTGGCATA | 840 |
| GGCCAAAACA | AAGAACATGA | TTGGGGTGTA | TTACCTGAAA | AATCAAGACC | AGCAAATTCC | 900 |
| TTCCACATAG | | | | | | 910 |

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGCCAAGTCA | TCCAACAAGT | CCAGAACGGT | TCTGGGGCTT | GGGATCCTCA | GTCGCTGGAG | 60 |
| ATAACTCCTT | TGGGCTTGTT | CATCATGTAG | TAGACAAACT | CTTCATACTC | CAACACTTGC | 120 |
| CCATCAAAAG | CGAATCTCAT | CTATTTTTTC | ATCAATCTGC | AATTTAGCTG | ATTTTTCTTT | 180 |
| TTTACCATT | ACAGTCACGC | GCCCAGCCTT | GAGCAAGTTT | TTGACCTCAG | TCCGACTTCC | 240 |
| CACCGCACAG | GCAACTAAAA | ATTTATCTAA | TCTCATAGAA | CTATTATATC | ATATCAAAAG | 300 |
| GAGGCTGGTA | CAATGACCAA | CCTCCTTTTC | GTTTCATACT | CTTCAAAAAT | CTCTTCAAAC | 360 |
| CGCGTCAACG | TCGCCTTGCC | GTATATATGT | TACTGACTTC | GTCAGTTCTA | TCTGCAACCT | 420 |
| CAAAGCAGTG | CTTTGAGCAA | CCTGCGGCTA | GTTTCCTAGT | TTGCTCTTTG | ATTTTCATTG | 480 |
| AGTATCAGAT | TTAGGAAATT | AACTTCCTCG | TCTCCAAAAA | ATAGCTAAGA | CAATCATGGC | 540 |
| ACCTAAACA | GCTGGGATAA | TAGCTGTTCC | TGATAAAACT | GGCCCCCAAG | TTCCAAAGAG | 600 |
| CAAGTGACCT | AGAAAGGCTC | CGATCCAACC | GAGAAACATT | TTTCCAAAAC | ATCCCATTGC | 660 |
| CTCTCCACGA | TTGGTCATAG | CACCTGCTAA | AAATCCCACT | AGGAGACCAA | CGAACATACT | 720 |
| TCCTAACATA | TTATCTCCTT | AATTTGCCCA | ATTCCCATT | CGGAAAAGAA | GTACTCGCGT | 780 |
| TCCATCTCA | CGAATACCAT | CGATATCCAT | TTGGTTAGAA | CCAATCATAA | AGTATACGTG | 840 |
| AACATCTGAA | CGGTTAAGCC | CTGCAG | | | | 866 |

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTTCAGGATG | TGGGAAAACG | ACCCTTCTTC | GTATGATTGC | AGGTTTCAAC | AGTATCAAAG | 60 |
| ATGGAGAATT | TACTTCGAT | GATACAAAAA | TCAATAATAT | GGAACCCAGC | AAACGCAATA | 120 |
| TCGGGCTGGT | TTTCCAAAAC | TACGCTATTT | TCCCACATTT | GACTGTCCGA | GACAACGTTG | 180 |
| CTTTTGGTCT | TATGCAAAAG | AAGGTTCCAA | AAGAAGAATT | GATTCAACAG | ACCAACAAGT | 240 |
| ATCTTGGACT | CATGCAAATT | GCTCAATATG | CGGATCGAAA | GCCCCGATAA | CTCAGTGGTG | 300 |
| GACAACAACA | ACGTGTCACC | TTGGCATGCG | TCTTAGCGGT | TAATCCAAGT | GTTCTCCTCC | 360 |
| ATGGACGAAG | CCACTTAGTA | ATCTGGAGGC | CAAACCTTCG | TTGGATATGC | GTTCAAGCCC | 420 |
| ATCCCAGAG | ATCCAACCAC | GAAGTTGGGG | AATTACAAC | GTTTATGTAA | CCCACGACCA | 480 |
| AGAAGGAGCC | ATGGCTATTT | CAGACCAAAT | TGCTGTAT | GAAAGATGGG | GTGATCCAAC | 540 |
| AAATCGGCCG | ACCAAAAGAA | CTGTATCATA | AACCAGCTAA | TGAGTTAGTG | GCAACCTTTA | 600 |
| TCGGACGCAC | AAATATTATC | CCTGCCAATC | TTGAAAACG | GAGCGACGGC | GNTTATATCG | 660 |
| TCTNTTCAGA | TGGANANGCC | CTTCGAATGA | TAG | | | 693 |

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

Met Ser Met Phe Thr Met Val Lys Met Asn Pro Leu Arg Gly Leu Ile
 1             5             10             15
Cys Asn Leu Lys Gly Asn Lys Ile Thr Ala Leu Ile Gly Pro Ser Gly
      20             25             30
Ser Gly Lys Ser Thr Tyr Leu Arg Ser Leu Asn Arg Met Asn Asp Thr
      35             40             45
Ile Asp Ile Ala Lys Val Thr Gly Gln Ile Leu Tyr Arg Gly Ile Asp
      50             55             60
Val Asn Arg Pro Glu Ile Asn Val Tyr Glu Met Arg Lys His Ile Gly
      65             70             75             80
Met Val Phe Gln Arg Pro Asn Pro Phe Ala Lys Ser Ile Tyr Arg Asn
      85             90             95
Ile Thr Phe Ala His Glu Arg Ala Gly Val Lys Asp Lys Gln Val Leu
      100            105            110
Asp Glu Ile Val Glu Thr Ser Leu Ser Gln Ala Ala Leu Trp Asp Gln
      115            120            125
Val Lys Asp Asp Leu His Lys Ser Ala Leu Thr Leu Ser Gly Gly Gln
      130            135            140
Gln Gln Arg Leu Cys Ile Ala Arg Ala Ile Ser Val Lys Pro Asp Ile
      145            150            155            160
Leu Leu Met Asp Glu Pro Ser Leu Ser Leu Gly Ser Asp Cys Asp His
      165            170            175
Ala Thr Arg Arg Asp His Val
      180

```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```

Met Ile Lys Ile Ser Asn Leu Ser Lys Ser Phe Ser Gly Gln Thr Val
 1           5           10           15
Leu Asp His Leu Asn Leu Asp Ile Gln Lys Gly Glu Val Val Ala Leu
      20           25           30
Ile Gly Ser Ser Gly Ala Gly Lys Ser Thr Phe Leu Arg Ser Leu Asn
 35           40           45
Tyr Leu Glu Thr Pro Asp Ser Gly Ser Ile Gln Ile Asp Gly Phe Ser
 50           55           60
Val Asp Phe Ser Lys Ile Thr Gln Glu Glu Ile Leu Ala Leu Arg Arg
 65           70           75           80
Lys Leu Ser Met Val Phe Gln Gln Phe Asn Leu Phe Glu Arg Arg Thr
      85           90           95
Ala Leu Asp Asn Val Lys Glu Gly Leu Val Val Val Lys Lys Leu Ser
 100           105           110
Asp Gln Glu Ala Thr Lys Ile Ala Lys Glu Glu Leu Ala Lys Val Gly
 115           120           125
Leu Ser Asp Arg Glu Asn His Tyr Pro Arg His Leu Ser Gly Gly Gln
 130           135           140
Lys Gln Arg Val Ala Leu Ala Arg Ala Leu Ala Met Lys Pro Asp Val
 145           150           155           160
Leu Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu Val Gly
      165           170           175
Glu Val Glu Lys Ser Ile Ala Asp Ala Ala Lys Ser Gly Gln Thr Met
 180           185           190
Ile Leu Val Ser His Asp Met Pro Phe Val Ala Gln Val Ala Asp Lys
 195           200           205
Ile Leu Phe Leu Asp Lys Gly Lys Ile Ile Glu Ser Gly Thr Pro Asp
 210           215           220
Glu Ile Ile His Thr Pro Lys Glu Glu Arg Thr Lys Glu Phe Phe Thr
 225           230           235           240
Ser Tyr Lys Arg Thr Tyr Ile
      245

```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```

Met Phe Ser Leu Arg Ser Val Phe Asp Gly Ile Pro Arg Ile Val Gln
 1           5           10           15
Gln Leu Pro Thr Thr Ile Met Leu Thr Ile Gly Gly Ala Leu Phe Gly
      20           25           30
Leu Val Leu Ala Leu Leu Phe Ala Ile Val Lys Ile Asn Arg Val Lys
      35           40           45
Ile Leu Tyr Pro Leu Gln Ala Phe Phe Val Ser Phe Leu Lys Gly Thr
      50           55           60
Pro Ile Leu Val Gln Leu Met Leu Thr Tyr Tyr Gly Ile Pro Leu Ala
      65           70           75           80
Leu Lys Ala Leu Asn Gln Gln Trp Gly Thr Gly Leu Asn Ile Asn Ala
      85           90           95
Ile Pro Ala Ala Ala Phe Ala Ile Val Ala Phe Ala Phe Asn Glu Ala
      100          105          110
Ala Tyr Ala Ser Glu Thr Ile Arg Ala Ala Ile Leu Ser Val Asn Pro
      115          120          125
Gly Glu Ile Glu Ala Ala Arg Ser Leu Gly Met Thr Arg Ala Gln Val
      130          135          140
Tyr Arg Arg Val Ile Ile Pro Asn Ala Ala Val Val Ala Thr Pro Thr
      145          150          155          160
Leu Ile Asn Ser Leu Ile Gly Leu Thr Lys Gly Thr Ser Leu Ala Phe
      165          170          175
Ser Ala Gly Val Val Glu Val Phe Ala Gln Ala Gln Ile Leu Gly Gly
      180          185          190
Ala Asp Tyr Arg Tyr Phe Glu Arg Phe Ile Ser Val Ala Leu Val Tyr
      195          200          205
Trp Val Val Asn Ile Gly Ile Glu Ser Leu Gly Arg Phe Ile Glu Arg
      210          215          220
Lys Met Ala Ile Ser Ala Pro Asp Thr Val Gln Thr Asp Val Lys Gly
      225          230          235          240
Asp Leu Arg

```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```

Met Tyr Arg Ile Asp Asp Asp Glu Gln Phe Val Leu Asp Phe Leu Lys
 1             5             10             15
Gln Glu Lys Val Leu Leu Val His Gly Arg Gly Phe Asn Trp Gln Glu
 20             25             30
Pro Asp His Phe Arg Ile Val Tyr Leu Pro Arg Val Asp Glu Leu Ala
 35             40             45
Gln Ile Gln Glu Lys Met Thr Arg Phe Leu Lys Gln Tyr Arg Arg
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Met Asn Asp Glu Ala Ser Lys Gln Leu Thr Asp Ala Arg Phe Lys Arg
 1             5             10             15
Leu Val Gly Val Gln Arg Thr Thr Phe Glu Glu Ile Leu Ala Val Leu
 20             25             30
Lys Thr Ala Tyr Gln Leu Lys His Ala Lys Gly Gly Arg Lys Pro Lys
 35             40             45
Leu Ser Leu Glu Asp Leu Leu Met Ala Thr Leu Gln Tyr Val Arg Glu
 50             55             60
Tyr Arg Thr Tyr Glu Gln Ile Ala Ala Asp Phe Gly Ile His Glu Ser
 65             70             75             80
Asn Leu Ile Arg Arg Ser Gln Trp Val Glu Val Thr Leu Val Gln Ser
 85             90             95
Gly Val Thr Ile Ser Arg Thr Pro Leu Ser Ser Glu Asp Thr Val Met
100             105             110
Ile Asp Ala Thr Glu Val Gln Ile Asn Arg Pro Lys Lys Arg Ile Ser
115             120             125

```

Glu Ser Phe Trp
130

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Met Arg Arg Lys Tyr Lys Ser Ile Ala Leu Lys Lys Glu Leu Ala Asn
 1             5             10             15
His Ser Gly Lys Lys Phe His Ala Met Lys Ala Gln Ala Ile Val
      20             25             30
Thr Ser Gln Gly Arg Ile Val Ser Leu Asp Ile Ala Val Asn Tyr Ser
      35             40             45
His Asp Met Lys Leu Phe Lys Met Ser Cys Arg Asn Ile Gly Gln Ala
      50             55             60
Gly Lys Ile Leu Ala Asp Ser Gly Tyr Gln Gly Pro Met Lys Ile Tyr
65             70             75             80
Pro Gln Ala Gln Thr Pro Arg Lys Ser Ser Lys Leu Lys Pro Leu Ile
      85             90             95
Ala Glu Asp Lys Ala Tyr Asn His Ala Leu Ser Lys Glu Arg Ser Lys
      100            105            110
Val Glu Asn Ile Phe Ala Lys Val Lys Thr Phe Lys Met Phe Ser Thr
      115            120            125
Thr Tyr Arg Asn His Arg Lys Arg Phe Gly Leu Arg Met Asn Leu Ile
      130            135            140
Ala Gly Ile Ile Asn Tyr Glu Leu Gly Phe
145            150

```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

Met Val Ser Ser Ser Gly Ser Glu Phe Gln Ser Gly Trp Gln Glu His
 1             5             10             15
Gln Leu Ile Ala Glu Lys Val Ser Lys Thr Leu Asp Lys Thr Phe Asp
             20             25             30
Lys Asp Val Arg Lys Ile Pro Thr Ser Pro Val Leu Ser Lys Ile Cys
             35             40             45
Arg

```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

Met Ile Lys Ile Leu Ala Ala Cys Gly Ala Gly Val Asn Ser Ser His
 1             5             10             15
Gln Ile Lys Ser Ala Leu Glu Glu Glu Leu Ser Asn Arg Gly Tyr Asp
             20             25             30
Val His Cys Asp Ala Val Met Val Lys Asp Val Asn Glu Asp Leu Met
             35             40             45
Lys Gly Tyr Asp Ile Phe Thr Pro Ile Ala Ala Thr Asp Leu Gly Phe
             50             55             60
Glu Pro Gly Ile Pro Val Ile Glu Ala Gly Pro Ile Leu Phe Arg Ile
             65             70             75             80
Pro Ala Met Ser Ala Pro Val Phe Asp Asn Ile Arg Leu Pro Ala Lys
             85             90             95
Gln Asn Met Val
             100

```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

Met Asn Thr Lys Met Met Ser Gln Phe Ser Val Met Asp Asn Glu Met
 1             5             10             15
Leu Ala Cys Val Glu Gly Gly Asp Ile Asp Trp Gly Arg Glu Ile Ser
      20             25             30
Cys Ala Ala Gly Val Ala Tyr Gly Ala Ile Asp Gly Cys Ala Thr Thr
      35             40             45
Val
  
```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

Met Arg Glu Lys Glu Ile Phe Asp Ser Ile Val Thr Ile Ile Gln Glu
 1             5             10             15
Arg Gln Gly Glu Asp Phe Val Val Thr Glu Ser Leu Ser Leu Lys Asp
      20             25             30
Asp Leu Asp Ala Asp Ser Val Asp Leu Met Glu Phe Ile Leu Thr Leu
      35             40             45
Glu Asp Glu Phe Ser Ile Glu Ile Ser Asp Glu Glu Ile Asp Gln Leu
      50             55             60
Gln Ser Val Gly Asp Val Val Lys Ile Ile Gln Gly Lys
      65             70             75
  
```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

Met Ala His Gly Asp Leu Leu Tyr His Asp Gly Leu Phe Phe Ser Ala
 1             5             10             15
Lys Lys Glu Asp Gly Thr Tyr Asp Phe His Glu Asn Phe Glu Tyr Val
             20             25             30
Thr Pro Trp Leu Lys Gln Val Asp
             35             40

```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

Met Ser Leu Ile Thr His Arg Arg Phe Ile Ser Cys Asn Glu Asn Ile
 1             5             10             15
Lys His Tyr Lys Arg Leu Ile Asp Lys Ala Glu Lys Cys Val Asn Asp
             20             25             30
Leu Met Ala Glu Leu Asn Ser Val Ile Thr Thr Val Thr Gly Ile Glu
             35             40             45
Asn Arg Leu Gly Ala Val Ile Leu Ala Glu Ile Arg Asn Ile His Ala
             50             55             60
Phe Asp Asn Pro Ala Gln Leu Gln Ala Phe Ala Gly Leu Asp Ser Ser
             65             70             75             80
Ile Tyr Gln Ser Gly Gln Ile Asp Leu Val Gly Arg Met Val Lys Arg
             85             90             95
Gly Ser Leu His Leu Arg
             100

```

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```

Met Ile Arg Ala Val Phe Phe Ser Ile Asp Asn Asp Met Glu Glu Ala
 1             5             10             15
Ala Arg Ser Met Gly Ala Ser Ser Phe Tyr Thr Met Val Arg Val Ile
          20             25             30
Ile Pro Tyr Ile Leu Pro Val Val Leu Ser Val Val Val Leu Asn Phe
          35             40             45
Asn Ser Leu Leu Ser Asp Tyr Asp Leu Ser Val Phe Leu Tyr His Pro
          50             55             60
Leu Phe Gln Pro Leu Gly Ile Val Ile Lys Gln Ser Thr Asp Glu Thr
          65             70             75             80
Ala Thr Leu Asn Ala Gln Ala Met Met Phe Val Tyr Ser Val Ile Leu
          85             90             95
Met Ile Met Ser Ser Ala Ala Leu Tyr Leu Ser Ser Leu Phe Gln Gly
          100             105             110
Lys Arg Gly Lys Arg
          115

```

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

```

Met Glu Lys Cys Tyr Thr Asp Val Thr Glu Phe Ala Ile Pro Ala Ser
 1             5             10             15
Thr Gln Lys Leu Tyr Leu Ser Pro Val Leu Asp Gly Phe Asn Ser Glu
          20             25             30

```

```

Ile Ile Ala Tyr Asn Leu Ser Thr Ser Pro Asn Leu Glu Gln Val Gln
  35                               40                               45
Thr Met Leu Glu Gln Ala Phe Thr Glu Lys His Tyr Glu Asn Thr Ile
  50                               55                               60
Leu His Ser Asp Gln Gly Trp Gln Tyr Gln His Asp Ser Tyr His Arg
  65                               70                               75                               80
Phe Leu Arg Val Arg Glu Phe Lys His Leu Cys His Ala Arg Glu Thr
                               85                               90                               95
Ala Lys Thr Thr Val
                               100

```

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

```

Met Glu Ile Leu Thr Thr Gln Gln Val Arg Glu Gly Tyr Gln Ala Ile
  1                               5                               10                               15
Leu Ala Ser Pro Leu Gly Leu Gln Asp Ala Phe Glu Val Ala Gln Glu
                               20                               25                               30
Lys Ser Gly Ser Tyr Thr Val Pro Pro Glu Ile Asp Gly Trp Lys Gly
  35                               40                               45
Asn Thr Glu Pro Leu Arg Ile Asp Tyr Val Phe Thr Thr Lys Glu Leu
  50                               55                               60
Ala Val Glu Asn Leu His Val Val Phe Asp Gly Asn Lys Ser Pro Gln
  65                               70                               75                               80
Val Ser Asp His Tyr Gly Leu Asn Ala Met Leu Asn Trp Lys
                               85                               90

```

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```

Met Leu Lys His Leu Asn Leu Lys Gly His Leu Leu Thr Ala Ile Ser
 1           5           10           15
Tyr Met Ile Pro Ile Val Cys Gly Ala Gly Phe Leu Val Ala Ile Gly
      20           25           30
Leu Ala Met Gly Gly Gly Val Pro Asp Ala Leu Val Ala Gly Lys Phe
      35           40           45
Thr Ile Trp Asp Ala Leu Ala Thr Met Gly Gly Lys Ala Leu Gly Leu
      50           55           60
Leu Pro Val Val Ile Ala Thr Gly Leu Ser Tyr Ser Ile Ala Gly Lys
      65           70           75           80
Pro Gly Ile Ala Pro Gly Phe Val Val Gly Leu Ile Ala Asn Ser Val
      85           90           95
Gly Ser Gly Phe Ile Gly Gly Ile Leu Gly Gly Tyr Ile Val Gly Phe
      100           105           110
Leu Val Gln Ala Ile Ile Lys Lys Val Lys Val Pro Asn Trp Ile Lys
      115           120           125
Gly Leu Met Pro Thr Leu Ile Ile Pro Phe Val Pro Leu Trp
      130           135           140

```

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

Met Ile Ala Leu Gly Trp Ser Asn Ile Gly Ala Ala Ile Ala Pro Asp
 1           5           10           15
Ala Ala Leu Ala Ser Val Ala Ala Ala Ile Ile Met Val Leu Gly Gly
      20           25           30
Asp Phe Thr Lys Thr Gly Ile Gly Val Ala Gln Ala Val Ala Ile Pro
      35           40           45
Leu Ala Val Ala Gly Leu Phe Leu Thr Met Ile Val Arg Thr Ile Ser
      50           55           60

```

Val Gly Leu Val His Thr Ala Asp Ala Ala Lys Lys Gly Asp Phe
 65 70 75 80
 Gly Ala Val Glu Arg Ala His Phe Ile Ala Leu Leu Phe Gln Gly Leu
 85 90 95
 Arg Ile Ala Leu Pro Ala Ala Leu Leu Leu Met Val Pro Thr Glu Thr
 100 105 110
 Val Gln Ser Ile Leu Ser Ala Met Pro Asp Trp Leu Lys Asp Gly Met
 115 120 125
 Ala Ile Gly Gly Gly Met Val Val Ala Val Gly Tyr Ala Met Val Ile
 130 135 140
 Asn Met Met Ala Thr Arg Glu Val Trp Pro Phe Phe Ala Leu Gly Phe
 145 150 155 160
 Val Leu Ala Ala Val Ser Asp Ile Thr Leu Ile Gly Phe Gly Ala Ile
 165 170 175
 Gly Val Ala Ile Ala Leu Ile Tyr Leu His Leu Ser Lys Thr Gly Gly
 180 185 190
 Asn Gly Gly Gly Gly Ala Ala Thr Ser Asn Asp Pro Ile Gly Asp Ile
 195 200 205
 Leu Glu Asp Tyr
 210

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Leu Asp Val Glu Ala Ile Arg Lys Asp Phe Pro Ile Leu Asp Gln
 1 5 10 15
 Ile Val Asn Asp Glu Pro Leu Val Tyr Leu Asp Asn Ala Ala Thr Thr
 20 25 30
 Gln Lys Pro Leu Val Val Leu Lys Ala Ile Asn Ser Tyr Tyr Glu Gln
 35 40 45
 Asp Asn Ala Asn Val His Arg Gly Val His Thr Leu Ala Glu Arg Ala
 50 55 60
 Thr Ala Ser Leu
 65

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

```

Met Thr Lys Leu Leu Asn Lys Lys Trp Lys Val Lys Ile Met Lys Gln
 1             5             10             15
Ile Leu Leu Val Cys Asn Ala Gly Met Ser Thr Ser Met Leu Val Lys
      20             25             30
Lys Met Gln Gln Ser Ala Thr Glu Arg Gly Ile Glu Ile Ser Ile Gln
      35             40             45
Ala Lys Ser Met Thr Glu Ala Lys Lys Asn Ile His Glu Ala Asp Val
      50             55             60
Ile Leu Ile Gly Pro Gln Ile Arg Tyr Glu Leu Leu Ala Val Lys Glu
65             70             75             80
Ile Ala Gly Asn Ile Pro Val Asp Thr Ile Asp Met Arg Asp Tyr Gly
      85             90             95
Met Met Asn Gly Ala Lys Val Leu Glu Gln Ala Leu Glu Trp Ile Gly
      100            105            110
Glu Ile Arg
      115

```

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

```

Met Val Leu Met Gln Lys Met His Gly Lys Glu Leu Ile Thr Leu Asn
 1             5             10             15

```

Gln Thr Val Lys Trp Tyr Lys Val Ser Gly Phe Met Ile Leu Leu Thr
 20 25 30
 Lys Pro Trp Tyr Tyr Leu Lys Ser Asp Gly Ser Tyr Ala Arg Asn Ala
 35 40 45
 Trp Gln Gly Asn Tyr Tyr Leu Lys Ser Asp Gly Lys Met Ala Val Asn
 50 55 60
 Glu Trp Val Tyr Asp Ala Thr Tyr Gln Ala Trp Tyr Tyr Leu Thr Ser
 65 70 75 80
 Asp Gly Ser Tyr Ala Tyr Ser Thr Trp Gln Gly Asn Tyr Tyr Pro Lys
 85 90 95
 Ile Gly Trp

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Leu Thr Val His Gly Lys Glu Ile Thr Ile Leu Lys Ser Asp Gly
 1 5 10 15
 Lys Met Ala Val Asn Glu Trp Val Asp Gly Gly Arg Tyr Tyr Val Gly
 20 25 30
 Ala Asp Gly Val Trp Lys Glu Gly Gln Ala Ser Thr Ala Ser Pro Ser
 35 40 45
 Asn Asp Ser Asn Ser Glu Tyr Ser Cys Cys Phe Arg Lys Gly Lys Lys
 50 55 60
 Leu
 65

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```

Met Asn Asn Asn Phe Asn Asn Phe Asn Asn Met Asp Asp Leu Phe Asn
 1             5             10             15
Gln Leu Met Gly Gly Met Arg Gly Tyr Ser Ser Glu Asn Arg Arg Tyr
 20             25             30
Leu Ile Asn Gly Arg Glu Val Thr Pro Glu Glu Phe Ala His Tyr Arg
 35             40             45
Thr Thr Gly Gln Leu Pro Gly Asn Ala Glu Thr Asp Val Gln Met Pro
 50             55             60
Gln Gln Ala Ser Gly Met Lys Gln Asp Gly Val Leu Ala Lys Leu Gly
 65             70             75             80
Arg Asn Leu Thr Ala Glu Ala Arg Glu Gly Lys Leu Asp Pro Val Ile
 85             90             95
Gly Arg Asn Lys Glu Ile Gln Glu Thr Ser Glu Ile Leu Ser Arg Arg
100             105             110
Thr Lys Asn Asn Pro Val Leu Val Gly Asp Ala Gly Val Gly Lys Thr
115             120             125
Ala Val Val Glu Gly Leu Ala Gln Ala Ile Val Asn Gly Asp Val Pro
130             135             140
Ala Ala Ile Lys Asn Lys Glu Ile Ile Ser Ile Asp Ile Ser Gly Leu
145             150             155             160
Glu Ala Gly Thr Gln Tyr Arg Gly Ser Phe Glu Glu Asn Val Gln Asn
165             170             175
Leu Val Asn Glu Val Lys Glu Ala Gly Asn Ile Ile Leu Phe Phe Asp
180             185             190
Glu Ile His Gln Ile Leu Gly Ala Gly Ser Thr Cys Gly Asp Ser Gly
195             200             205
Ser Lys Gly Leu Ala Asp Ile Leu Ser Gln Ser Ile Ser Leu Val Glu
210             215             220
Asn
225

```

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```

Met Thr Ile Phe Pro Asp Asp Phe Leu Trp Gly Gly Ala Val Ala Ala
 1           5           10           15
Asn Gln Val Glu Gly Ala Tyr Asn Glu Asp Gly Lys Gly Leu Ser Val
          20           25           30
Gln Asp Val Leu Pro Lys Gly Gly Leu Gly Glu Ala Thr Glu Asn Pro
      35           40           45
Thr Glu Asp Asn Leu Lys Leu Ile Gly Ile Asp Phe Tyr His Lys Tyr
      50           55           60
Lys Glu Asp Ile Ser Leu Phe Ser Glu Met Gly Phe Asn Val Phe Arg
      65           70           75           80
Thr Ser Ile Ala Trp Ser Arg Ile Phe Pro Lys Gly Asp Glu Glu Glu
          85           90           95
Pro Asn Glu Ala Gly Leu Lys Tyr Tyr Asp Glu Leu Phe Asp Glu Leu
          100          105          110
His Ala His Gly Ile Glu Pro Leu Val Thr Leu Ser His Tyr Glu Thr .
          115          120          125
Pro Leu Tyr Leu Ala Arg Lys Tyr His Gly Trp Ile Asp Arg Lys Asn
          130          135          140
Asp Ser Phe Leu
145

```

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```

Met Ile Glu Tyr Lys Asn Val Ala Leu Arg Tyr Thr Glu Lys Asp Val
 1           5           10           15
Leu Arg Asp Val Asn Leu Gln Ile Glu Asp Gly Glu Phe Met Val Leu
          20           25           30
Val Gly Pro Ser Gly Ser Gly Lys Thr Thr Met Leu Lys Met Ile Asn
          35           40           45
Arg Leu Leu Glu Pro Thr Asp Gly Asn Ile Tyr Met Asp Gly Lys Arg
          50           55           60

```

```

Ile Lys Asp Tyr Asp Glu Arg Glu Leu Arg Leu Ser Thr Gly Tyr Val
65          70          75          80
Leu Gln Ala Ile Ala Leu Phe Pro Asn Leu Thr Val Ala Glu Asn Ile
          85          90          95
Ala Leu Ile Pro Glu Met Lys Gly Trp Ser Lys Glu Glu Ile Thr Lys
          100         105         110
Lys Thr Glu Glu Leu Leu Ala Lys Val Gly Leu Pro Val Ala Glu Tyr
          115         120         125
Gly His Arg Leu Pro Ser Glu Leu Ser Gly Gly Glu Gln Gln Arg Val
          130         135         140
Gly Ile Val Arg Ala Met Ile Gly Gln Pro Lys Ile Phe Leu Met Asp
145          150          155          160
Glu Pro Phe Ser Ala Leu Asp Ala Ile Ser Arg Lys Gln Leu Gln Val
          165         170         175
Leu Thr Lys Glu Leu His Lys Glu Phe Gly Met Thr Thr Ile Phe Val
          180         185         190
Thr His Asp Thr Asp Glu Ala Leu Lys Leu Ala Asp Arg Ile Ala Val
          195         200         205
Leu Gln Asp Gly Glu Ile Arg Gln Val Ala Asn Pro Glu Thr Ile Leu
          210         215         220
Lys Val Pro Ala Thr Asp Phe Val Ala Asp Leu Phe Gly Gly Ser Val
225          230          235          240
His Asp

```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```

Met Pro Phe Val Pro Gly Ile Ala Leu Thr Asn Ala Val Arg Asp Ile
1          5          10          15
Met Thr Asn His Ile Asn Ser Gly Met Ser Lys Met Phe Glu Ser Leu
          20          25          30
Leu Ile Thr Leu Ala Leu Gly Ala Gly Thr Ser Val Ala Leu Val Leu
          35          40          45

```

Met Asn

50

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```

Met Tyr Thr Ile Arg Met Leu Lys Met Gly Ser Glu Ala Ala Ala Lys
 1             5             10             15
Ser Ala Gln Glu His Gly Leu Lys Ser Val Glu Val Thr Val Lys Gly
             20             25             30
Pro Gly Ser Gly Arg Glu Ser Ala Ile Ser Cys Ala Cys Cys Arg Trp
          35             40             45
Ser

```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```

Met Ile Glu Phe Glu Lys Pro Asn Ile Thr Lys Ile Asp Glu Asn Lys
 1             5             10             15
Asp Tyr Gly Lys Leu Val Ile Glu Pro Leu Glu Arg Gly Tyr Gly Thr
             20             25             30
Ala Leu Gly Asn Ser Leu Arg Arg Val Leu Leu Ala Ser Leu Pro Gly
          35             40             45
Ala Ala Val Thr Ser Ile Asn Ile Asp Gly Val Leu His Glu Phe Asp
          50             55             60

```

```

Thr Val Pro Gly Val Arg Glu Asp Val Met Gln Ile Ile Leu Asn Ile
65              70              75              80
Lys Gly Ile Ala Val Lys Ser Tyr Val Glu Asp Glu Lys Ile Ile Glu
              85              90              95
Leu Asp Val Glu Gly Pro Ala Glu Val Thr Ala Gly Asp Ile Leu Thr
              100             105             110
Asp Ser Asp Ile Glu Ile Val Asn Pro Asp His Tyr Leu Phe Thr Ile
              115             120             125
Gly Glu Gly Ser Ser Leu Lys Ala Thr Met Thr Val Asn Ser Gly Arg
              130             135             140
Gly Tyr Val Pro Ala Asp Glu Asn Lys Lys Asp Asn Ala Pro Val Gly
145              150              155              160
Thr Leu Ala Val Asp Ser Ile Tyr Thr Pro Val Thr Lys Val Asn Tyr
              165              170              175
Gln Val Glu Pro Ala Arg Val Gly Ser Asn Asp Gly Phe Asp Lys Leu
              180             185             190
Thr Leu Glu Ile Leu Thr Asn Gly Thr Ile Ile Pro Glu Asp Ala Leu
              195             200             205
Gly Leu Ser Ala Arg Ile Leu Thr Glu His Leu Asp Leu Phe Thr Asn
              210             215             220
Leu Thr Glu Ile Ala Lys Ser Thr Glu Val Met Lys Glu Ala Asp Thr
225              230              235              240
Glu Ser Asp Asp Arg Ile Leu Asp Arg Thr Ile Glu Glu Leu Asp Leu
              245              250              255
Ser Val Arg Ser Tyr Asn Cys Leu Lys Arg Ala Gly Ile Asn Thr Val
              260             265             270
His Asp Leu Thr Glu Lys Ser Glu Ala Glu Met Met Lys Val Arg Asn
              275             280             285
Leu Gly Arg Lys Ser Leu Glu Glu Val Lys Leu Lys Leu Ile Asp Leu
              290             295             300
Gly Leu Gly Leu Lys Asp Lys
305              310

```

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

```

Met Asp Ile Glu Lys Gln Arg Gly Ile Ser Val Thr Ser Ser Val Met
 1             5             10             15
Gln Phe Asp Tyr Asp Gly Lys Arg Val Asn Ile Leu Asp Thr Pro Gly
      20             25             30
His Glu Asp Phe Ser Glu Asp Thr Tyr Arg Thr Leu Met Ala Val Asp
      35             40             45
Ala Ala Val Met Val Val Asp Ser Ala Lys Gly Ile Glu Ala Gln Thr
      50             55             60
Lys Lys Leu Phe Glu Val Val Lys His Arg Gly Ile Pro Val Phe Thr
65             70             75             80
Phe Met Asn Lys Leu Asp Arg Asp Gly Arg Glu Pro Leu Asp Leu Leu
      85             90             95
Gln Glu Leu Glu Glu Ile Leu Gly Ile Ala Ser Tyr Pro Met Asn Trp
      100            105            110
Pro Ile Gly Met Gly Lys Ala Phe Glu Gly Leu Tyr Asp Leu Tyr Asn
      115            120            125
Gln Arg Leu Glu Leu Tyr Lys Gly Asp Glu Arg Phe Ala Ser Pro Arg
      130            135            140
Arg Trp Arg Gln Thr Phe Trp
145            150

```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```

Met Ala Val Ile Ala Glu Arg Lys Ala Tyr Tyr His Asp Pro Val Glu
 1             5             10             15
Asp Ala Ile Ile Met Lys Arg Glu Ile Asp Glu Gly
      20             25

```

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```

Met Asn Glu Thr Trp Ser Arg Thr Ala Leu Thr Leu Leu Lys His Gly
 1             5             10             15
Ser Glu Val Asn Leu Glu Arg Ala Leu Ser Val Asn Gly Arg Leu Gly
             20             25             30
Gly His Val Val Thr Gly His Ile Asp Gly Thr Gly Lys Ile Ser Ser
             35             40             45
Ile Lys Lys Asp Asp Asn Ala Val Trp Tyr Gln Ile Asn Thr Gln Lys
             50             55             60
Glu Ile Leu Asp Leu Ile Val Glu Lys Gly Ser Ile Thr Ile Asp Gly
65             70             75             80
Ile Ser Leu Thr Val Ala Lys Val Ser Lys Val Asn Phe Ser Val Ser
             85             90             95
Val Ile Pro His Thr Leu Lys Gln Thr Ile Leu Lys Ser Lys Gln Val
             100            105            110
Gly Ser Thr Val Asn Leu Glu Asn Asp Ile Leu Gly Lys Tyr Val Gln
             115            120            125
Lys Leu Met Asp Asn Ser Pro Lys Ser Glu Ile Ser Lys Glu Leu Leu
             130            135            140
Tyr Gln Asn Gly Phe
145

```

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```

Met Asn Trp Ser Ala Leu Glu Gln Gln Ile Val Asp Glu Leu Lys Ile
 1             5             10             15
Tyr Ile Ala Pro Lys Ile Phe Gly Gly Ser Ala Lys Phe Pro Val Gly
             20             25             30

```

Gly Glu Gly Ile Ser Leu Pro Asn Asp Ala Ile Arg Leu Lys Pro Tyr
 35 40 45
 Ala Phe Ser Gln Xaa Gly Xaa Asp Tyr Leu Ile Glu Ser Glu Val Ile
 50 55 60
 Tyr Pro Cys Ser Gln Glu
 65 70

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Met Val Leu Phe Leu Val Pro Gln Leu Arg Asn Ala Tyr Gly Thr Ala
 1 5 10 15
 Ala Ile Gly Ile Ile Cys Gly Leu Tyr Trp Ala Val Ser Ser Asn Met
 20 25 30
 Thr Val Glu Ala Thr Gln Arg Leu Thr Gly Gly Gly Gly Phe Ala Ile
 35 40 45
 Gly His Gln Gln Gln Phe Ala Ile Trp Phe Val Asp Lys Val Ala Gly
 50 55 60
 Arg Phe Gly Lys Lys Glu Glu Ser Leu Asp Asn Leu Lys Leu Pro Lys
 65 70 75 80
 Phe Leu Ser Ile Phe His Asp Thr Val Val Ala Ser Ala Thr Phe Asp
 85 90 95
 Ala Arg Ile Leu Arg Gly His Ser Phe Asn Leu Gly Ser Arg His Tyr
 100 105 110
 Val

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```

Met Leu Ile Asn Ser Leu Asn Gln Ser Tyr Ile Ser Ala Lys Arg Ile
 1           5           10           15
Glu Glu Val Phe Ala Glu Ser Pro Glu Asn Ile His Ser Glu Leu Glu
 20           25           30
Gln Lys Gln Val Thr Ser Gly Arg Val Leu Gln Val Gln Glu Leu Thr
 35           40           45
Phe Thr Tyr Pro Asp Ala Ala Gln Pro Ser Leu Arg Asp Ile Ser Phe
 50           55           60
Asp Met Thr Gln Gly Gln Ile Leu Gly Ile Ile Gly Gly Thr Gly Ser
 65           70           75           80
Gly Lys Ser Ser Leu Val Gln Leu Leu Leu Gly Leu Tyr Pro Val Asp
 85           90           95
Lys Gly Asn Ile Asp Leu Tyr Gln Asn Gly Arg Ser Pro Leu Asn Leu
100          105          110
Glu Gln Trp Arg Ser Trp Ile Ala Tyr Val Pro Gln Lys Val Lys Leu
115          120          125
Phe Lys Gly Thr Ile Arg Ser Asn Leu Thr Leu Gly Leu Asn Gln Glu
130          135          140
Val Ser Asp Gln Lys Leu Trp Gln Ala Leu Glu Ile Ala Gln Ala Lys
145          150          155          160
Asp Phe Val Ser Glu Lys Glu Gly Leu Leu Asp Ala Leu Ile Glu Ala
165          170          175
Gly Gly Arg Asn Phe Ser Gly Gly Gln Lys Gln Arg Leu Ser Ile Ala
180          185          190
Arg Ala Val Leu Arg Gln Ala Pro Phe Ile Ile Leu Asp Asp Ala Thr
195          200          205
Ser Ala Leu Asp Thr Ile Thr Glu Ser Lys Leu Leu Lys Ala Ile Arg
210          215          220
Glu Asn Phe Pro Asn Thr Ser Leu Ile Leu Ile Ser Gln Arg Thr Ser
225          230          235          240
Thr Leu Gln Met Ala Asp Gln Ile Leu Leu Leu Glu Lys Gly Glu Leu
245          250          255
Leu Ala Val Gly Lys His Asp Asp Leu Met Lys Ser Ser Gln Val Tyr
260          265          270
Arg Glu Ile Asn Ala Ser Gln His Gly Lys Glu Asp
275          280

```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```

Met Lys Asp Pro Glu Ser Arg Leu Tyr Ile Leu Leu Lys Asp Gly Gln
 1             5             10             15
Val Ile Gly Thr Cys Thr Val Asp Leu Ser Thr Asn Thr Asn Tyr Phe
             20             25             30
Tyr Gly Leu Ala Ile Leu Glu Pro Glu Arg Gly Lys Gly Tyr Gly Ser
             35             40             45
Tyr Leu Ala Lys Ser Leu Val Asn Gln Leu Ile Glu Gln Asn Asp Lys
             50             55             60
Glu Phe Gln Ile Ala Val Glu Asp Ser Asn Val Gly Ala Lys Arg Leu
65             70             75             80
Tyr Glu Lys Ile Gly Phe Val Lys Gln Thr Gln Val Val Tyr Leu Asn
             85             90             95
Glu Lys Gly Ala Arg Asp Ser Glu Val
             100             105

```

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```

Met Phe Ala Leu Ser Ser Asn Lys Glu Leu Ala Glu Arg Val Ala Gln
 1             5             10             15
Glu Ile Gly Ile Glu Leu Gly Lys Ser Ser Val Arg Gln Phe Ser Asp
             20             25             30
Gly Glu Ile Gln Val Asn Ile Glu Glu Ser Ile Arg Gly Lys His Val
             35             40             45
Phe Ile Leu Gln Ser Thr Ser Ser Pro Val Asn Asp Asn Leu Leu Glu
50             55             60

```

Ile Leu Ile Met Val Asp Ala Leu Lys Arg Ala Ser Ala Glu Ser Val
 65 70 75 80
 Asn Val Val Met Pro Tyr Tyr Gly Tyr Ala Arg Gln Asp Arg Lys Ala
 85 90 95
 Arg Ala Arg Glu Pro Ile Thr Ser Lys Leu Val Ala Asn Met Leu Glu
 100 105 110
 Val Ala Gly Val Asp Arg Leu Leu Thr Ile Asp Leu His Ala Ala Gln
 115 120 125
 Ile Gln Gly Phe Phe Asp Ile Pro Val Asp His Leu Met Gly Ala Pro
 130 135 140
 Leu Ile Ala Asp Tyr Phe Glu Arg Pro Gly Met Val Gly Ser Asp Tyr
 145 150 155 160
 Val Val Val Ser Pro Asp His Gly Gly Val Thr Arg Ala Arg Lys Leu
 165 170 175
 Ala Glu Phe Leu Lys Thr Ser Ile Ala Ile Ile Glu Lys Arg Arg Ser
 180 185 190
 Val Asp Lys Met Asn Thr Ser Glu Val Met Asn Thr Ile Gly Lys Val
 195 200 205
 Glu Gly Asn His Leu
 210

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Met Ile Ser Phe Leu Leu Leu Leu Val Leu Val Trp Gly Phe Tyr Ile
 1 5 10 15
 Gly Tyr Arg Arg Gly Leu Leu Leu Gln Val Tyr Tyr Leu Ile Ser Ala
 20 25 30
 Met Ala Ser Ala Phe Met Ala Gly Gln Phe Tyr Lys Gly Leu Gly Glu
 35 40 45
 Gln Phe His Leu Leu Leu Pro Tyr Ala Asn Ser Gln Glu Gly Gln Gly
 50 55 60
 Thr Phe Phe Phe Pro Ser Asp Gln Leu Phe Gln Leu Asp Lys Val Phe
 65 70 75 80

```

Tyr Ala Gly Ile Gly Tyr Leu Leu Val Phe Gly Ile Val Tyr Ser Ile
      85                      90                      95
Gly Arg Leu Leu Gly Leu Leu Leu His Leu Ile Pro Ser Lys Lys Leu
      100                    105                    110
Gly Gly Lys Leu Phe Gln Val Ser Ala Gly Ile Leu Ser Met Leu Val
      115                    120                    125
Thr Leu Phe Val Leu Gln Met Ala Leu Thr Ile Leu Ala Thr Ile Pro
      130                    135                    140
Met Ala Val Ile Gln Asn Pro Leu Glu Lys Ser Ile Val Ala Lys His
      145                    150                    155                    160
Ile Ile Gln Ser Ile Pro Ile Thr Thr Ser Trp Leu Lys Gln Ile Trp
      165                    170                    175
Val Thr Asn Leu Ile Gly
      180

```

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```

Met Arg Ala Phe Ser Asp Phe Gly Thr Pro Met Leu Ile Gly Glu Gly
  1              5              10              15
Tyr Arg Thr Phe Pro Val Leu Ile Tyr Thr Gln Phe Ile Ser Glu Val
      20              25              30
Gly Gly Asn Ser Ala Phe Ala Ile Met Ala Ile Ile Ala Leu Ala
      35              40              45
Ile Phe Leu Ile Gln Lys His Ile Ala Asn Arg Tyr Ser Phe Ser Met
      50              55              60
Asn Leu Leu His Pro Ile Glu Pro Lys Lys Thr Thr Lys Gly Lys Met
      65              70              75              80
Ala Ala Ile Tyr Ala Thr Val Tyr Gly Ile Ile Phe Ile Ser Val Leu
      85              90              95
Pro Gln Ile Tyr Leu Ile Tyr Thr Ser Phe Leu Lys Thr Ser Gly Met
      100             105             110
Val Phe Val Lys Gly Tyr Ser Pro Asn Ser Tyr Lys Val Ala Phe Asn
      115             120             125

```

Arg Met Gly Ser Ala Ile Phe Asn Thr Ile Arg Ile Pro Leu Ile Ala
 130 135 140
 Leu Val Leu Val Val Pro Ile Tyr Asp Ile Tyr Leu Leu Pro Ser Arg
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Met Val Pro Tyr Ile Val Pro Gly Thr Val Leu Gly Ile Ala Phe Ile
 1 5 10 15
 Ser Ser Phe Asn Thr Gly Leu Phe Gly Ser Gly Phe Leu Met Ile Thr
 20 25 30
 Gly Thr Ala Phe Ile Leu Ile Met Ser Leu Ser Val Arg Arg Leu Pro
 35 40 45
 Tyr Thr Ile Arg Ser Ser Val Ala Ser Leu Gln Gln Ile Ala Pro Ser
 50 55 60
 Ile Glu Glu Ala Ala Gly Lys Leu Arg Lys
 65 70

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met Ile Phe Ile Pro Met Ala Ala Tyr Ser Ile Ala Arg Asn Met Ser
 1 5 10 15
 Lys Arg Lys Ala Phe Thr Ile His Val Tyr Pro Leu Asn Pro Arg Asn
 20 25 30

Leu Arg Thr Phe Pro Ser His His Asp Ser Asp Tyr Gly Tyr Asp Glu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Met Lys Phe Arg Lys Leu Ala Cys Thr Val Leu Ala Gly Ala Ala Val
 1 5 10 15
 Leu Gly Leu Ala Ala Cys Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala
 20 25 30
 Lys Ser Gly Gly Asp Gly Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe
 35 40 45
 Pro Val Phe Thr Gln Glu Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu
 50 55 60
 Lys Ser Ile Ile Gln Ala Phe
 65 70

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Met Asn Ser Gln Gln Lys Pro Gln Glu Ile Lys Val Glu Glu Pro Val
 1 5 10 15
 Glu Ser Lys Glu Glu Thr Val Asn Gln Pro Val Glu Gln Pro Lys Val
 20 25 30
 Glu Thr Pro Ala Val Glu Lys Gln Thr Glu Pro Thr Glu Glu Pro Lys
 35 40 45

```

Val Glu Val Thr Ser Ile Pro Gln Thr Thr Arg Tyr Glu Glu Asp Leu
  50                      55                      60
Thr Lys Glu His Gly Thr Arg Glu Val Val Lys Glu Gly Lys Asn Gly
  65                      70                      75                      80
Ser Arg Thr Val Thr Thr Pro Tyr Ile Leu Asn Ala Thr Asp Gly Thr
                      85                      90                      95
Thr Thr Glu Gly Thr Ser Thr Thr Asp Glu Ala Glu Met Glu Lys Glu
                      100                      105                      110
Val Val Arg Val Gly Thr Lys Pro Lys Glu Lys Leu Ala Pro Val Leu
                      115                      120                      125
Ser Leu Thr Ser Val Thr Asp Asn Ala Met Leu Arg Ser Ala Arg Leu
                      130                      135                      140
Thr Tyr His Leu Glu Asn Thr Asp Ser Val Asp Val Lys Lys Ile His
                      145                      150                      155                      160
Ala Glu Ile Lys Asn Gly Asp Lys Val Val Lys Thr Ile Asp Leu Ser
                      165                      170                      175
Lys Glu Arg Leu Ser Asp Ala Val Asp Gly Leu Glu Leu Tyr Lys Asp
                      180                      185                      190
Tyr Lys Ile Val Thr Ser Met Thr Tyr Asp Arg Gly Asn Gly Glu Glu
                      195                      200                      205
Thr Ser Thr Leu Glu Glu Thr Pro Leu Arg Leu Asp Leu Lys Lys Val
                      210                      215                      220
Glu Leu Lys Asn Ile Gly Ser Thr Asn Leu Val Lys Val Asn Glu Asp
                      225                      230                      235                      240
Gly Thr Glu Val Ala Ser Asp Phe Leu Thr Ser Lys Pro Val Asp Val
                      245                      250                      255
Gln Asn Tyr Tyr Leu Lys Val Thr Ser Arg Asp Asn Lys Val Val Ser
                      260                      265                      270
Pro Pro Ser
                      275

```

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

```

Met Ala Val Met Lys Ile Glu Tyr Tyr Ser Gln Val Leu Asp Met Glu
 1              5              10              15
Trp Gly Val Asn Val Leu Tyr Pro Asp Ala Asn Arg Val Glu Glu Pro
      20              25              30
Glu Cys Glu Asp Ile Pro Val Leu Tyr Leu Leu His Gly Met Ser Gly
      35              40              45
Asn His Asn Ser Trp Leu Lys Arg Thr Asn Val Glu Arg Leu Leu Arg
      50              55              60
Gly Thr Asn Leu Ile Val Val Met Pro Asn Thr Ser Asn Gly Trp Tyr
      65              70              75              80
Thr Asp Thr Gln Tyr Gly Phe Asp Tyr Tyr Thr Ala Leu Ala Glu Glu
      85              90              95
Leu Pro Gln Val Pro Glu Thr Leu Leu Pro
      100              105

```

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

```

Met Arg Leu Leu Ala Met Lys Met Lys Gln Ile Ser Asp Thr Thr Leu
 1              5              10              15
Lys Ile Thr Met Ser Leu Glu Asp Leu Met Asp Arg Gly Met Glu Ile
      20              25              30
Ala Asp Phe Leu Val Pro Gln Glu Lys Thr Glu Glu Phe Phe Tyr Ala
      35              40              45
Ile Leu Gly
      50

```

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```

Met Leu Pro Ile Ile Cys Cys Gly Glu Ser Leu Glu Thr Tyr Glu Ala
 1             5             10             15
Gly Lys Ala Ala Glu Phe Val Gly Ala Gln Val Ser Ala Ala Leu Ala
      20             25             30
Gly Leu Thr Ala Glu Gln Val Ala Ala Ser Val Ile Ala Tyr Glu Pro
      35             40             45
Ile Trp Ala Ile Gly Thr Gly Lys Ser Ala Ser Gln Asp Asp Ala Gln
      50             55             60
Lys Met Cys Lys Val Val Arg Asp Val Val Ala Ala Asp Phe Gly Gln
      65             70             75             80
Glu Val Ala Asp Lys Val Arg Val Gln Tyr Gly Gly Ser Val Lys Pro
      85             90             95
Glu Asn Val Ala Ser Tyr Met Ala Cys Pro Asp Val Asp Gly Ala Leu
      100            105            110
Val Gly Gly Ala Ser Leu Glu Ala Glu Ser Phe Leu Ala Leu Leu Asp
      115            120            125
Phe Val Lys
      130

```

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

```

Met Phe Val Glu Ala Cys Lys Ala Val Val Arg Ala Asn Glu Glu Tyr
 1             5             10             15
Val Pro Pro Tyr Gly Ile Gly Gly Thr Leu Tyr Leu Arg Pro Leu Leu
      20             25             30
Ile Gly Val Gly Asp Ile Ile Gly Val Lys Pro Ala Glu Glu Tyr Ile
      35             40             45
Phe Thr Ile Phe Ala Met Pro Val Gly Asn Tyr Phe Lys Gly Gly Leu
      50             55             60

```

```

Val Pro Thr Asn Phe Leu Ile Gln Asp Glu Tyr Asp Arg Ala Ala Pro
65          70          75          80
Asn Gly Thr Gly Ala Ala Lys Val Gly Gly Asn Tyr Ala Ala Ser Leu
          85          90          95
Leu Pro Gly Lys Met Ala Lys Ser Arg His Phe Ser Asp Val Ile Tyr
          100          105          110
Leu Asp Pro Ser Thr His Thr Lys Ile Glu Glu Val Gly Ser Ala Asn
          115          120          125
Phe Phe Gly Ile Thr Ala Asp Asn Glu Phe Val Thr Pro Leu Ser Pro
          130          135          140
Ser Ile Leu Pro Ser Ile Thr Lys Tyr Ser Leu Leu Tyr Leu Ala Glu
145          150          155          160
His Arg Leu Gly Leu Thr Pro Ile Glu Gly Asp Val Pro Ile Asp Asn
          165          170          175
Leu Asp Arg Phe Val Lys Ala Gly Ala Cys Gly Thr Ala Ala Val Ile
          180          185          190
Ser Pro Ile Gly Gly Ile Gln His Gly Asp Asp Phe His Val Ile Leu
          195          200          205

```

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

```

Met Val Met Ile Ser Met Leu Phe Tyr Ser Glu Thr Glu Val Gly Pro
1          5          10          15
Val Thr Arg Lys Leu Tyr Asn Glu Leu Thr Gly Ile Gln Phe Gly Asp
          20          25          30
Ile Glu Ala Pro Glu Gly Trp Ile Val Lys Val Asp
          35          40

```

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

```

Met Thr Ala Ser Pro Leu Lys Lys Ser Ile Lys Lys Lys Asn Arg Lys
 1           5           10           15
Leu Thr Asn Lys Xaa Glu Lys His Met Ser Lys Ile Ile Gly Ile Asp
          20           25           30
Leu Gly Thr Thr Asn Ser Ala Val Ala Val Leu Glu Gly Thr Glu Ser
          35           40           45
Lys Ile Ile Ala Asn Pro Glu Gly Asn Arg Thr Thr Pro Ser Val Val
          50           55           60
Ser Phe Lys Asn Gly Glu Ile Ile Val Gly Asp Ala Ala Lys Arg Gln
65           70           75           80
Ala Val Thr Asn Pro Asp Thr Val Ile Ser Ile Lys Ser Lys Met Gly
          85           90           95
Thr Ser Glu Lys Val Ser Ala Asn Gly Lys Glu Tyr Thr Pro Gln Glu
          100          105          110
Ile Ser Ala Met Ile Leu Gln Tyr Leu Lys Gly Tyr Ala Glu Asp Tyr
          115          120          125
Leu Gly Glu Lys Val Thr Lys Ala Val Ile Thr Val Pro Ala Tyr Phe
          130          135          140
Asn Asp Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Lys Ile Ala Gly
145          150          155          160
Leu Glu Val Xaa Arg Ile Val Asn Glu Pro Thr Ala Ala Ala Leu Ala
          165          170          175
Tyr Gly Leu Asp Lys Thr Asp Lys Glu Glu Lys Ile Leu Val Phe Asp
          180          185          190
Leu Gly Gly Gly Thr Phe Asp Val Ser Ile Leu Glu Leu Gly Asp Gly
          195          200          205
Val Phe Asp Val Leu Ser Thr Ala Gly Asp Asn Lys Leu Gly Gly Asp
          210          215          220
Asp Phe Asp Gln Lys Ile Ile Asp His Leu Val Ala Glu Phe Lys Lys
225          230          235          240
Glu Asn Gly Ile Arg Leu Val Tyr
          245

```

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

```

Met Lys Leu Ile Val Asp Leu Ile Tyr Glu Gly Gly Phe Lys Lys Met
 1             5             10             15
Arg Gln Ser Ile Ser Asn Thr Ala Glu Tyr Gly Asp Tyr Val Ser Gly
      20             25             30
Pro Arg Val Ile Thr Glu Gln Val Lys Glu Asn Met Lys Ala Val Leu
      35             40             45
Ala Asp Ile Gln Asn Gly Lys Phe Ala Asn Asp Phe Val Asn Asp Tyr
      50             55             60
Lys Ala Gly Arg Pro Lys Leu Thr Ala Tyr Arg Glu Gln Ala Ala Asn
      65             70             75             80
Leu Glu Ile Glu Lys Val Gly Ala Glu Leu Arg Lys Ala Met Pro Phe
      85             90             95
Val Gly Lys Asn Asp Asp Asp Ala Phe Lys Ile Tyr Asn
      100             105

```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

```

Met Leu Leu Ser Ala Phe His Lys Tyr Glu Asn Gln Leu Asp Lys Val
 1             5             10             15
Arg Phe Ile Gly Leu His Thr Gly His Leu Gly Phe Tyr Thr Asp Tyr
      20             25             30
Arg Asp Phe Glu Leu Asp Lys Leu Val Thr Asn Leu Gln Leu Asp Thr
      35             40             45
Gly Ala Arg Val Ser Tyr Pro Val Leu Asn Val Lys Val Phe Leu Glu
      50             55             60
Asn Gly Glu Val Lys Ile Phe Arg Ala Leu Asn Glu Ala Ser Ile Arg
      65             70             75             80

```

Arg Ser Asp Arg Thr Met Val Ala Asp Ile Val Ile Asn Gly Val Pro
 85 90 95
 Phe Glu Arg Phe Arg Gly Asp Gly Leu Thr Val Ser Thr Pro Thr Gly
 100 105 110
 Ser Thr Ala Tyr Asn
 115

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met Gly Ala Gln Leu Ala Arg Glu Phe Lys His Glu Ala Asp Ile Val
 1 5 10 15
 Val Gly Val Pro Asn Ser Ser Leu Ser Ala Ala Met Gly Phe Ala Glu
 20 25 30
 Glu Ser Gly Leu Pro Asn Glu Met Gly Leu Ile Lys Asn Gln Tyr Thr
 35 40 45
 Gln Arg Thr Phe Ile Gln Pro Thr Gln Glu Leu Arg Glu Gln Gly Val
 50 55 60
 Arg Met Lys Leu Ser Ala Val Ser Gly Val Val Lys Gly Lys Arg Val
 65 70 75 80
 Val Met Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Arg Arg Ile
 85 90 95
 Val Gln Leu Leu Lys Glu Ala Gly Ala Thr Glu Val His Val Ala Ile
 100 105 110
 Gly Ser Pro Ala Leu Ala Tyr Pro Cys Phe Tyr Gly Ile Asp Ile Gln
 115 120 125
 Thr Arg Gln Glu Leu Ile Ala Ala Asn His Thr Val Glu Glu Thr Arg
 130 135 140
 Gln Ile Ile Gly Ala Asp Ser Leu Thr Tyr Leu Ser Ile Asp Ser Leu
 145 150 155 160
 Ile Glu Ser Ile Gly Ile Glu Thr Asp Ala Pro Asn Gly Gly Leu Cys
 165 170 175
 Val Ala Tyr Phe Asp Gly Asp Tyr Pro Thr Pro Leu Tyr Asp Tyr Glu
 180 185 190

Glu Asp Tyr Arg Arg Ser Leu Glu Glu Lys Thr Ser Phe Tyr Lys
 195 200 205

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met Lys Ile Leu Val Thr Gly Phe Asn Pro Phe Gly Gly Glu Lys Ile
 1 5 10 15
 Asn Pro Ala Leu Glu Ala Val Lys Leu Leu Pro Ser Glu Ile Asn Gly
 20 25 30
 Ala Glu Val Arg Trp Val Glu Ile Pro Thr Val Phe Tyr Lys Ser Ser
 35 40 45
 Glu Val Leu Glu Ala Glu Ile Leu Arg Tyr Gln Pro Asp Ala Val Leu
 50 55 60
 Cys Ile Gly Gln Ala Gly Gly Arg Thr Gly Leu Thr Pro Glu Arg Val
 65 70 75 80
 Ala Ile Asn Gln Asp Asp Ala Arg Ile Pro Asp Asn Glu Gly Asn Gln
 85 90 95
 Pro Ile Asp Thr Pro Ile Arg Ile Asp Gly Ala Ser Ala Tyr Phe Ser
 100 105 110
 Ser Leu Pro Ile Lys Ala Met Val Gln Ala Asn Lys Lys Glu Gly Leu
 115 120 125
 Thr Gly Ser Leu Phe Pro Ile Arg Ala Gly Thr Phe Val Cys Ser His
 130 135 140
 Leu Met Tyr Gln Ala Leu Tyr Leu Val Glu Lys Lys Phe Pro Tyr Val
 145 150 155 160
 Lys Ala Gly Phe Met His Ile Pro Tyr Met Met Glu Gln Val Val Asn
 165 170 175
 Arg Pro Thr Thr Pro Thr Met Ser Leu Val Asp Ile Arg Arg Gly Ile
 180 185 190
 Glu Ala Ala Ile Gly Ala Met Ile Glu His Gly Asp Gln Glu Leu Thr
 195 200 205
 Leu Val Gly Gly Glu Ile His
 210 215

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```

Met Leu Val Pro Lys Arg Val Lys His Arg Arg Glu Phe Arg Gly Lys
 1             5             10             15
Met Arg Gly Glu Ala Lys Gly Gly Lys Glu Val Ala Phe Gly Glu Tyr
          20             25             30
Gly Leu Gln Ala Thr Thr Ser His Trp Ile Thr Asn Arg Gln Ile Glu
          35             40             45
Ala Ala Arg Ile Ala Met Thr Arg Tyr Met Lys Arg Gly Gly Lys Val
          50             55             60
Trp Ile Lys Ile Phe Pro His Lys Ser Tyr Thr Ala Lys Ala Ile Gly
65             70             75             80
Val Arg Met Gly Ser Gly Lys Gly Ala Pro Glu Gly Trp Val Ala Pro
          85             90             95
Val Lys Arg Gly Lys Val Met Phe Glu Ile Ala Gly Val Ser Glu Glu
          100            105            110
Ile Ala Arg Glu Ala Leu Arg Leu Ala Ser His Lys Leu Pro Val
          115            120            125

```

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```

Met Gly Trp Trp Arg Glu Thr Ile Asp Ile Val Lys Glu Asn Asp Pro
 1             5             10             15

```

```

Ala Ala Arg Thr Thr Leu Glu Val Leu Leu Thr Tyr Pro Gly Val Lys
      20                      25                      30
Ala Leu Ala Ala His Arg Leu Ser His Phe Leu Trp Lys Tyr Asp Phe
      35                      40                      45
Lys Leu Leu Ala Arg Met His Ser Gln Phe Trp Arg Phe Trp Thr Gln
      50                      55                      60
Ile Glu Ile His Pro Gly Ala Gln Ile Asp Ser Gly Val Phe Ile Asp
      65                      70                      75                      80
His Gly Ser Gly Leu Val Ile Gly Glu Thr Ala Ile Val Glu Lys Gly
      85                      90                      95
Val Leu Leu Tyr His Gly Val Thr Leu Gly Gly Thr Gly Lys Asp Cys
      100                     105                     110
Gly Lys Arg His Pro Thr Val Arg Lys Gly Ala Leu Ile Ser Ala His
      115                     120                     125
Ala Gln Val Ile Gly Pro Val Glu Ile Gly Glu Asn Ala Lys Val Gly
      130                     135                     140
Ala Ala Ala Val Val Val Ala Asp Val Pro Ser Asp Val Thr Val Val
      145                     150                     155                     160
Gly Ile Pro Ala Lys Ile Val Arg Leu His Gly Lys Lys Asp Glu Pro
      165                     170                     175
Val Ile His Glu Val Glu Glu Lys Arg Glu Tyr Tyr Val Asn Lys Leu
      180                     185                     190
Glu Gln Ala Lys Asp Ala Ser His Arg Ser Ser Gly Leu
      195                     200                     205

```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

Met Leu Phe Tyr Leu Leu Arg Asp Gly Lys Gly Leu Arg Asn Tyr Leu
  1                      5                      10                      15
Thr Gln Phe Ile Pro Ser Lys Leu Lys Glu Pro Val Gly Gln Val Leu
      20                      25                      30
Ser Asp Val Asn Gln Gln Leu Ser Asn Tyr Val Arg Gly Gln Val Thr
      35                      40                      45

```

```

Val Ala Ile Ile Val Ala Val Met Phe Ile Ile Phe Phe Lys Ile Ile
  50                      55                      60
Gly Leu Arg Tyr Ala Val Thr Leu Gly Val Thr Ala Gly Ile Leu Asn
  65                      70                      75                      80
Leu Val Pro Tyr Leu Gly Ser Phe Leu Ala Met Leu Pro Ala Leu Val
                      85                      90                      95
Leu Gly Leu Ile Ala Gly Pro Val Met Leu Leu Lys Val Val Ile Val
                      100                      105                      110
Phe Ile Val Glu Gln Thr Ile Glu Gly Arg Phe Val Ser Pro Leu Ile
                      115                      120                      125
Leu Gly Ser Gln Leu Asn Ile His Pro Ile Asn Val Leu Phe Val Leu
                      130                      135                      140
Leu Thr Ser Gly Ser Met Phe Gly Ile Trp Gly Val Leu Leu Gly Ile
  145                      150                      155                      160
Pro Val Tyr Ala Ser Ala Lys Val Val Ile Ser Ala Ile Phe Glu Trp
                      165                      170                      175
Tyr Lys Val Val Ser Gly Leu Tyr Glu Leu Glu Gly Glu Glu Val Lys
                      180                      185                      190
Ser Glu Gln
                      195

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Met Thr Lys Gln Val Pro Lys Phe Thr Lys Asp Thr Ala Gln Leu Tyr
  1                      5                      10                      15
Thr Cys Lys Trp Leu Leu Tyr Asn Lys Val Thr Lys Met Tyr Asp His
                      20                      25                      30
Thr Val Val Asn His Ser Val Arg Glu Tyr Ile Thr Asp Ser Ile Ser
                      35                      40                      45
Thr Asn Thr Ile Glu Glu Thr Gly
  50                      55

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

```

Met Lys Lys Arg Ala Ile Val Ala Val Ile Val Leu Leu Leu Ile Gly
 1           5           10           15
Leu Asp Gln Leu Val Lys Ser Tyr Ile Val Gln Gln Ile Pro Leu Gly
          20           25           30
Glu Val Arg Ser Trp Ile Pro Asn Phe Val Ser Leu Thr Tyr Leu Gln
          35           40           45
Asn Arg Gly Ala Ala Phe Ser Ile Leu Gln Asp Gln Gln Leu Leu Phe
          50           55           60
Ala Val Ile Thr Leu Val Val Val Ile Gly Ala Ile Trp Tyr Leu His
65           70           75           80
Lys His Met Glu Asp Ser Phe Trp Met Val Leu Gly Leu Thr Leu Ile
          85           90           95
Ile Ala Gly Gly Leu Gly Asn Phe Ile Asp Arg Val Ser Gln Gly Phe
          100          105          110
Val Val Asp Met Phe His Leu Asp Phe Ile Asn Phe Ala Ile Phe Asn
          115          120          125
Val Ala Asp Asn Tyr Leu Thr Val Gly Val Ile Ile Leu Leu Ile Ala
          130          135          140
Met Leu Lys Glu Glu Ile Asn Gly Asn
145          150

```

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```

Met Gly Ala Tyr Tyr Leu Val Met Gln Ser Leu Ser Tyr Leu Glu Tyr
 1              5              10              15
Glu Gln Gly Ile Gln Ser Thr Thr Val Arg His Leu Ile Leu Val Phe
      20              25              30
Tyr Leu Leu Phe Phe Met Gly Gly Ile Lys Lys Leu Asp Thr Tyr Leu
      35              40              45
Lys Glu Lys Leu Gln Glu Glu Leu Asn Gln Glu Gln Thr Leu Arg Tyr
      50              55              60
Arg Asp Met Glu Arg Tyr Ser Arg His Ile Glu Glu Leu Tyr Lys Glu
65              70              75              80
Ile Arg Ser Phe Arg His Asp Tyr Thr Asn Leu Leu Thr Thr Tyr Val
      85              90              95
Trp Ala Leu Lys Arg Arg Ile Trp Ser Arg
      100              105

```

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```

Met His Val Arg Met Ile Pro Lys Ser Thr Pro Asp Thr Lys Phe Ala
 1              5              10              15
Asp Val Ala Thr His Gln Pro Glu Tyr Ser Arg Asp Asn Val Ala Gly
      20              25              30
Thr Ile Val Gly Phe Trp Thr Pro Glu Ile Phe His Gly Val Ser Val
      35              40              45
Ala Gly Tyr His Leu His Phe Ile Ser Asp Asp Leu Thr Phe Gly Gly
      50              55              60
His Val Met Asp Phe Val Ile Lys Glu Gly Ile Ile Glu Val Gly Ala
65              70              75              80
Val Asp Gln Leu Asp Gln Arg Phe Pro Val Gln Asp Arg Gln Tyr Leu
      85              90              95
Phe Ala Lys Phe Asn Val Asp Glu Met Lys Lys Asp Ile Glu Lys Ala
      100              105              110
Glu

```

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Met Ala Val Ala Lys Gly Lys Leu Thr Ile Ile Ala His Val Ala Cys
 1             5             10             15
Asn Asn Thr Lys Asp Ser Met Glu Leu Ala Arg His Ala Glu Ser Leu
          20             25             30
Gly Val Asp Ala Ile Ala Thr Asp Ser Thr Asn Leu Phe Pro Leu Ala
          35             40             45
Arg Ile Thr Gln Leu Pro Asn Thr Gly Thr Ile Ser Val Leu Gln Leu
          50             55             60
Gln Thr Gln Thr Thr
          65

```

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

Met Gly Glu Thr Gln Ile Ile Asp Gly Leu Asp Pro Glu Tyr Lys Lys
 1             5             10             15
Arg Phe Met His His Tyr Asn Phe Pro Gln Tyr Ser Val Gly Glu Thr
          20             25             30
Gly Arg Tyr Gly Ala Pro Gly Arg Arg Glu Ile Gly His Gly Ala Leu
          35             40             45
Gly Glu Arg Ala Leu Ala Gln Val Leu Pro Ser Leu Glu Glu Phe Pro
          50             55             60

```

Tyr Ala Ile Arg Leu Val Ala Glu Val Leu Glu Ser Asn Gly Ser Ser
 65 70 75 80
 Ser Gln Ala Ser Ile Cys Ala Gly Thr Leu Ala Leu Met Ala Gly Gly
 85 90 95
 Val Pro Ile Lys Ala Pro Val Ala Gly Ile Ala Met Gly Leu Ile Ser
 100 105 110
 Asp Gly Asn Asn Tyr Thr Val Leu Thr Asp Ile Gln Gly Leu Glu Asp
 115 120 125
 His Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Arg Asp Gly Ile
 130 135 140
 Thr Ala Leu Gln Met Asp Ile Lys Ile Gln Gly Ile Thr Ala Glu Ile
 145 150 155 160
 Leu Thr Glu Ala Leu Ala Gln Ala Lys Lys Ala Arg Phe Glu Ile Leu
 165 170 175
 Asp Val Ile Glu Ala Thr Ile Pro Glu Val Arg Pro Glu Leu Ala Pro
 180 185 190
 Thr Ala Pro Lys Ile Asp Thr Ile Lys Ile Asp Val Asp Lys Ile Lys
 195 200 205
 Ile Val Ile Gly Lys Gly Gly Glu Thr Ile Asp Lys Ile Ile Ala Glu
 210 215 220
 Thr Gly Val Lys Ile Asp Ile Asp Glu Glu Xaa Asn Val Phe Tyr Leu
 225 230 235 240
 Leu Leu Val Asp Gln Asn Ala Ile Asn Pro Cys Pro Lys Lys Leu Leu
 245 250 255
 Leu Val Trp Phe Arg Glu Pro Lys Trp Met Lys Phe Thr Val Leu Asn
 260 265 270
 Arg Ser Tyr Arg Glu Phe Gly Ala Phe Val Thr Leu
 275 280

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Met Ile Asn Asn Val Val Leu Val Gly Arg Met Thr Arg Asp Ala Glu
 1 5 10 15

```

Leu Arg Tyr Thr Pro Ser Asn Val Ala Val Ala Thr Phe Thr Leu Ala
      20                      25                      30
Val Asn Arg Thr Phe Lys Ser Gln Asn Gly Glu Arg Glu Ala Asp Phe
      35                      40                      45
Ile Asn Val Val Met Trp Arg Gln Gln Ala Glu Asn Leu Ala Asn Trp
      50                      55                      60
Ala Lys Lys Gly Ser Leu Ile Gly Val Thr Gly Arg Ile Gln Thr Arg
      65                      70                      75                      80
Ser Tyr Asp Asn Gln Gln Gly Gln Arg Val Tyr Val Thr Glu Val Val
      85                      90                      95
Ala Glu Asn Phe Gln Met Leu Glu Ser Arg Ser Val Arg Glu Gly His
      100                     105                     110
Thr Gly Gly Ala Tyr Ser Ala Pro Thr Ala Asn Tyr Ser Ala Pro Thr
      115                     120                     125
Asn Ser Val Pro Asp Phe Ser Arg Asn Glu Asn Pro Phe Gly Ala Thr
      130                     135                     140
Asn Pro Leu Asp Ile Ser Xaa Asp Asp Leu Pro Phe
      145                     150                     155

```

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

Met Asp Leu Val Arg Ile Leu Lys Glu Pro Arg Asn Ala Leu Val Lys
  1              5              10              15
Gln Tyr Gln Thr Leu Leu Ser Tyr Asp Asp Val Glu Leu Glu Phe Asp
      20              25              30
Asp Glu Ala Leu Gln Glu Ile Ala Asn Lys Ala Ile Glu Arg Lys Thr
      35              40              45
Gly Ala Arg Gly Leu Arg Ser Ile Ile Glu Glu Thr Met Leu Asp Val
      50              55              60
Met Phe Glu Val Pro Ser Gln Glu Asn Val Lys Leu Val Arg Ile Thr
      65              70              75              80
Lys Glu Thr Val Asp Gly Thr Asp Lys Pro Ile Leu Glu Thr Ala
      85              90              95

```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Met Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu Asn Ile Leu Leu
 1             5             10             15
Lys Leu Leu Gln Val Ala Asp Phe Asn Ile Glu Arg Ala Glu Arg Gly
      20             25             30
Ile Ile Tyr Val Asp Glu Ile Asp Lys Ile Ala Lys Lys Ser Glu Asn
      35             40             45
Val Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val Gln Gln Ala Leu
      50             55             60
Leu Lys Ile Ile Glu Gly Thr Val Ala Ser Val Pro Pro Gln Gly Gly
      65             70             75             80
Arg Lys His Pro Gln Gln Val Asp Asp Ser Ser Gly Tyr Lys Lys Tyr
      85             90             95
Pro Leu His Arg Gly Trp Cys Phe
      100

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

Met Trp Pro Arg Glu Ser Arg Ser Cys Arg Leu Thr Lys Val Lys Ile
 1             5             10             15

```

Cys Gly Leu Ser Thr Lys Glu Ala Val Glu Thr Ala Val Ser Ala Gly
 20 25 30
 Ala Asp Tyr Ile Gly Phe Val Phe Ala Pro Ser Lys Arg Gln Val Thr
 35 40 45
 Leu Glu Glu Ala Ala Glu Leu Ala Lys Leu Ile Pro Ala Asp Val Lys
 50 55 60
 Lys Val Gly Val Phe Val Ser Pro Ser Arg Val Glu Leu Leu Glu Ala
 65 70 75 80
 Ile Asp Lys Val Gly Leu Asp Leu Val Gln Val His Gly Gln Val Ala
 85 90 95
 Asp Asp Leu Phe Glu Asn Leu Pro Cys Ala Ser Ile Gln Ala Val Gln
 100 105 110
 Val Asp Gly Asn Gly His Val Pro Asn Ser Gln Ala Asp Tyr Leu Leu
 115 120 125
 Phe Asp Ala Pro Val Ala Gly Ser Gly Gln Ser Phe Asp Trp Gly Gln
 130 135 140
 Leu Asp Thr Thr Gly Leu Ala Gln Pro Phe Phe Ile Ala Gly Gly Leu
 145 150 155 160
 Asn Glu Asp Asn Val Val Lys Ala Ile Gln His Phe Thr Pro Tyr Ala
 165 170 175
 Val Asp Val Ser Ser Gly Val Glu Thr Asp Gly Gln Lys Asp His Glu
 180 185 190
 Lys Ile Arg Arg Phe Ile Glu Arg Val Lys His Gly Ile Ser Gly Thr
 195 200 205
 Lys

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Met Asn Cys Glu Ala Val Ala Leu Gly Ser Phe Cys Glu Leu Lys Ser
 1 5 10 15
 Arg Arg Gly Lys Lys Gln Lys Gly Glu Ile Leu Met Ala Val Ile Ser
 20 25 30

Met Lys Gln Leu Leu Glu Ala Gly Val His Phe Gly His Gln Thr Arg
 35 40 45
 Arg Trp Asn Pro Lys Met Ala Lys Tyr Ile Phe Thr Glu Arg Asn Gly
 50 55 60
 Ile His Val Ile Asp Leu Gln Gln Thr Val Lys Tyr Ala Asp Gln Ala
 65 70 75 80
 Tyr Xaa Phe Met Arg Asp Ala Ala Ala Asn Asp Ala Val Val Leu Phe
 85 90 95
 Val Gly Thr Lys Lys Thr Ser Ser
 100

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Met Val Asp Thr Asn Thr Asp Pro Asp Asp Ile Asp Val Ile Ile Pro
 1 5 10 15
 Ala Asn Asp Asp Ala Ile Arg Ala Val Lys Leu Ile Thr Ala Lys Leu
 20 25 30
 Ala Asp Ala Ile Ile Glu Gly Arg Gln Gly Glu Asp Ala Val Ala Val
 35 40 45

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Met Glu Glu Leu Gly Gln Ser Tyr Gly Tyr Leu Leu Tyr Arg Thr Glu
 1 5 10 15

```

Thr Asn Trp Asp Ala Glu Glu Glu Arg Leu Arg Ile Ile Asp Gly Arg
    20                      25                      30
Asp Arg Ala Gln Leu Tyr Val Asp Gly Gln Trp Val Lys Thr Gln Tyr
    35                      40                      45
Gln Thr Glu Ile Gly Glu Asp Ile Phe Tyr Gln Gly Lys Lys Lys Gly
    50                      55                      60
Leu Ser Arg Leu Asp Ile Leu Ile Glu Asn Met Gly Arg Val Asn Tyr
    65                      70                      75                      80
Gly His Lys Phe Leu Ala Asp Thr Gln Arg Lys Gly Ile Arg Thr Gly
                      85                      90                      95
Val Cys Lys Asp Leu His Phe Leu Leu Asn Trp Lys His Tyr Pro Leu
                      100                      105                      110
Pro Leu Asp Asn Pro Glu Lys Ile Asp Phe Ser Lys Gly Trp Thr Gln
                      115                      120                      125
Gly Gln Pro Ala Phe Tyr Ala Tyr Asp Phe Thr Val Glu
    130                      135                      140

```

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

```

Met Gly Lys Glu Lys Val Trp Leu Pro Arg Lys Gln Gly Leu Pro Gly
  1                      5                      10                      15
Leu Ala Tyr Tyr Val Ile Glu Val Ala His Lys Glu Glu Leu Leu Thr
    20                      25                      30
Ile Ala Gln Arg Ala Gln Glu Val Asp Val Pro Ile Lys Trp Met Thr
    35                      40                      45
Ser Ser Gln Leu Glu Ile Thr Asp Ser Asp Gly Ile Val Thr Cys Ile
    50                      55                      60
Arg Leu Ala Arg
    65

```

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

```

Met Asn Lys Lys Gln Trp Leu Gly Leu Gly Leu Val Ala Val Ala Ala
 1           5           10           15
Val Gly Leu Ala Ala Cys Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser
          20           25           30
Ser Ser Asp Val Lys Thr Lys Ala Ala Ile Val Thr Asp Thr Gly Gly
          35           40           45
Val Asp Asp Lys Ser Phe Asn Gln Ser Ala Trp Glu Val Ala Gly Leu
          50           55           60
Gly
65
  
```

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

```

Met Ser Gln Trp Asp Arg Lys Leu Asp Ala Arg Leu Ala Gln Ala Val
 1           5           10           15
Val Ser Ile Asn Ala Phe Lys Gly Val Glu Phe Gly Leu Gly Phe Glu
          20           25           30
Ala Gly Tyr Arg Lys Gly Ser Gln Val Met Asp Glu Ile Leu Trp Ser
          35           40           45
Lys Glu Asp Gly Tyr Thr Arg Arg Thr Asn Asn Leu Gly Gly Phe Glu
          50           55           60
Gly Gly Met Thr Asn Gly Gln Pro Ile Val Val Arg Gly Val Met Lys
          65           70           75           80
Pro Ile Pro Thr Leu Tyr Lys Pro Leu Met Ser Val Asp Ile Glu Thr
          85           90           95
  
```

His Glu Pro Tyr Lys Ala Thr Val Glu Arg Ser Asp Pro Thr Ala Leu
 100 105 110
 Pro Ala Ala Gly Met Val Met Glu Ala Val Val Ala Thr Val Leu Ala
 115 120 125
 Gln Glu Ile Leu Glu Lys Phe Ser Ser Asp Asn Leu Glu Glu Leu Lys
 130 135 140
 Glu Ala Val Ala Lys His Arg Asp Tyr Thr Lys Asn Tyr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Met Glu Asp Ser Asn Ser Phe Met Leu Ser His Gln Met Glu Thr Ile
 1 5 10 15
 Leu Lys Glu Ala Gly Phe Thr Lys Ala Val Ser Tyr Phe Ile Leu Glu
 20 25 30
 Leu Lys Asp Pro Ser Gln Thr Lys Val Val Thr Glu Glu Leu Gln Lys
 35 40 45
 Asn Lys Lys Tyr Thr Val Leu Ser
 50 55

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Met Gly Lys Lys Arg Trp Ala Arg Asn Gly Phe Glu Ser Asn Asp Ala
 1 5 10 15

Ser Tyr Ala Gln Val Val Ser Leu Tyr Asp Asp Thr Ser Ile Ser Val
 20 25 30
 Ser Asn Asn Glu Thr Asp Lys Val Leu Ala Gly Ser Leu Tyr Thr Asp
 35 40 45
 Thr Asn Glu Gln Gly Leu Thr Ile Pro Ser Ser Phe Thr Lys Lys Leu
 50 55 60
 Glu
 65

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met Ala Met Glu Ser Gly Ala Thr Ala Val Val Ala Glu Arg Gly Gln
 1 5 10 15
 Glu Arg Ile Thr Lys Val Arg Glu Ile Leu Gly Gly Gly Ala Asp Ala
 20 25 30
 Ala Leu Glu Cys Val Gly Thr Glu Ala Ala Ile Glu Gln Ala Leu Gly
 35 40 45
 Val Leu His Asn Gly Gly Arg Met Gly Phe Val Gly Val Pro His Tyr
 50 55 60
 Asn Asn Arg Ala Leu Gly Ser Thr Phe Met Gln Asn Ile Ser Val Ala
 65 70 75 80
 Gly Gly Ala Ala Ser Ala Thr Thr Tyr Asp Lys Gln Phe Leu Leu Lys
 85 90 95
 Ala Val Leu Asp Gly Asp Ile Asn Pro Gly Arg Val Phe Thr Ser Ser
 100 105 110
 Tyr Lys Leu Glu Asp Ile Asp Gln Ala Tyr Lys Asp Met Asp Glu Arg
 115 120 125
 Lys Thr Ile Lys Ser Met Ile Val Ile Glu
 130 135

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```

Met Lys Gln Val Val Asp Tyr Phe Leu Ser Gln Gly Met Asp Arg Ile
 1             5             10             15
Gly Ile Leu Thr Gly Leu Glu Glu Thr Thr Asp Gln Glu Glu Ile Ile
      20             25             30
Gln Asp Lys Arg Leu Glu Asn Phe Lys Asn Tyr Ser Gln Ala Arg Gly
      35             40             45
Ile Tyr His Asp Glu Leu Val Phe Gln Gly Arg Phe Thr Ala Gln Ser
      50             55             60
Gly Tyr Asp Leu Met Lys Glu Ala Ile Gln Ser Leu Gly Asp Gln Leu
65             70             75             80
Pro Pro Ala Phe Phe Ala Ala Ser Asp Ser Leu Ala Ile Gly Ala Leu
      85             90             95
Arg Ala Leu Gln Glu Ala Gly Ile Ser Leu Pro Asp Arg Val Ser Leu
      100            105            110
Ile Phe Leu Leu Thr Thr Leu Ser Leu Thr Lys Gln Val Tyr Pro Pro
      115            120            125
Leu Ser
      130
  
```

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

Met Ala Lys Val Thr Ile Met Leu Ala Cys Ala Ala Gly Met Ser Thr
 1             5             10             15
Ser Leu Leu Val Thr Lys Met Gln Lys Ala Ala Glu Asp Lys Gly Leu
      20             25             30
  
```

```

Asp Ala Glu Ile Phe Ala Val Pro Ala Pro Glu Ala Glu Glu Ile Val
  35                      40                      45
Ala Thr Lys Glu Val Asn Val Leu Leu Leu Gly Pro Gln Val Arg Tyr
  50                      55                      60
Leu Leu Gly Asp Phe Gln Glu Lys Leu Lys Asp Arg Gln Ile Pro Val
  65                      70                      75                      80
Ala Val Ile Pro Met Thr Asp Tyr Gly Met Met Asn Gly Ser Lys Val
                      85                      90                      95
Leu Asp Leu Ala Glu Ser Leu Leu Asp
                      100                      105

```

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

Met His Gly Ala Gly Val Asn Glu Pro Val Ala Glu Leu Ser Val Ala
  1                      5                      10                      15
Glu Gln Leu Leu Glu Ala Gly Ala Asp Val Ile Leu Val Pro Ala Val
                      20                      25                      30
Gly Thr Val Pro Ala Phe His Asp Gln Glu Leu Arg Glu Val Val Asp
                      35                      40                      45
Leu Val His Ser Lys Gly Gly Leu Val Leu Ser Ala Ile Gly Thr Ser
                      50                      55                      60
Gln Glu Thr Ser Asp Thr Asp Thr Ile Lys Glu Ile Ala Leu Arg Asn
                      65                      70                      75                      80
Lys Ile Cys Gly Val Asp Ile Gln His Ile Gly Asp Ala Gly Tyr Gly
                      85                      90                      95
Gly Leu Ala Thr Val Asp Asn Ile Tyr Ala Leu Ser Lys Ala Ile Arg
                      100                      105                      110
Gly Val Arg His Thr Val Ser Arg Leu Ala Arg Ser Val Asn Arg
                      115                      120                      125

```

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Ile | Asn | Leu | Ala | Ser | Val | Pro | Lys | Glu | Ser | Leu | Thr | Gln |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Leu | Pro | Arg | Asp | Leu | His | Ala | Glu | Tyr | Phe | Ala | Val | Leu | Ala | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ile | Ala | Thr | Ser | Ile | Glu | Arg | Met | Ala | Thr | Glu | Ile | Arg | Gly | Leu | Gln |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Lys | Ser | Glu | Gln | Arg | Glu | Val | Glu | Glu | Phe | Phe | Ala | Lys | Gly | Gln | Lys |
| | 50 | | | | 55 | | | | | | 60 | | | | |
| Gly | Ser | Ser | Ala | Met | Pro | His | Lys | Arg | Asn | Pro | Ile | Gly | Ser | Glu | Asn |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Met | Thr | Gly | Leu | Ala | Arg | Val | Ile | Arg | Gly | His | Met | Ile | Thr | Ala | Tyr |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Glu | Asn | Val | Ala | Leu | Trp | His | Glu | Arg | Asp | Ile | Ser | His | Ser | Ser | Ala |
| | | 100 | | | | | | 105 | | | | | 110 | | |
| Glu | Arg | Ile | Ile | Thr | Pro | Asp | Thr | Thr | Ile | Leu | Ile | Asp | Tyr | Met | Leu |
| | | 115 | | | | 120 | | | | | | 125 | | | |
| Asn | Arg | Phe | Gly | Asn | Ile | Val | Lys | Asn | Leu | Thr | Val | Phe | Pro | Glu | Asn |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Met | Ile | Arg | Asn | Met | Asn | Ser | Thr | Phe | Gly | Leu | Ile | Phe | Ser | Gln | Arg |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Ala | Met | Leu | Thr | Leu | Ile | Glu | Lys | Gly | Met | Thr | Arg | Glu | Gln | Ala | Tyr |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Asp | Leu | Val | Gln | Pro | Lys | Thr | Ala | Tyr | Ser | Trp | Asp | Asn | Gln | Val | Asp |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Phe | Lys | Pro | Leu | Leu | Glu | Ala | Asp | Ser | Glu | Val | Thr | Ser | Arg | Leu | Thr |
| | 195 | | | | | 200 | | | | | | 205 | | | |
| Gln | Glu | Glu | Ile | Asp | Glu | Ile | Phe | Asn | Pro | Val | Tyr | Tyr | Thr | Lys | Arg |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Val | Asp | Asp | Ile | Phe | Glu | Arg | Leu | Gly | Leu | Gly | Asp | | | | |
| 225 | | | | | | 230 | | | | | 235 | | | | |

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```

Met Leu Asn Leu Thr His Val Thr Leu Lys Thr Arg Gln Val Ile Leu
 1             5             10             15
Gln Asp Ala Asp Phe Thr Phe Lys Lys Gly Arg Ile Tyr Gly Leu Leu
          20             25             30
Ala Ile Asn Gly Ser Gly Lys Thr Thr Leu Phe Arg Ala Met Ser Lys
          35             40             45
Leu Leu Pro Leu Ser Ser Gly His Ile Ala Val Pro Pro Ser Leu Phe
          50             55             60
Tyr Tyr Glu Ser Val Glu Trp Leu Asp Gly Asn Leu Ser Gly Met Asp
65             70             75             80
Tyr Leu Arg Leu Ile Lys Lys His Leu Glu Val Arg Pro Lys Leu Glu
          85             90             95
Arg

```

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

Met Tyr Thr Leu Gly Gln Pro Asn Glu Leu Ala Ala Glu Phe Leu Asn
 1             5             10             15
Phe Val Leu Ser Asp Glu Thr Gln Glu Gly Ile Val Lys Gly Leu Lys
          20             25             30
Tyr Ile Pro Ile Lys Glu Met Lys Val Glu Lys Asp Ala Ala Gly Thr
          35             40             45
Val Thr Val Leu Glu Gly Arg Gln
          50             55

```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

Met Asn Gln Glu Glu Leu Ala Lys Lys Met Leu Leu Pro Ser Lys Asn
 1             5             10             15
Ser Arg Leu Glu Lys Leu Gly Lys Gly Leu Thr Phe Ala Cys Leu Ser
          20             25             30
Leu Ile Val Ile Leu Val Ala Met Ile Leu Val Phe Val Ala Gln Lys
          35             40             45
Gly Leu Ser Thr Phe Phe Val Asn Gly Val Asn Ile Phe Asp Phe Leu
          50             55             60
Leu Gly Gly Thr Trp Asn Pro Ser Ser Lys Glu Phe Gly Ala Leu Pro
65             70             75             80
Met Ile Leu Gly Ser Phe Ile Val Thr Ile Leu Ser Ala Leu Ile Ala
          85             90             95
Thr Pro Phe Ala Ile Gly Ala Ala Val Phe Met Thr Glu Val Ser Pro
          100            105            110
Lys Gly Ala Lys Ile Leu Gln Pro Ala Ile Glu Leu Leu Val Gly Ile
          115            120            125
Pro Ser Val Val Tyr Gly Phe Ile Gly Leu Gln Val Val Val Pro Phe
          130            135            140
Val Arg Ser Val Phe Gly Gly Thr Gly Phe Gly Ile Leu Ser Gly Ile
          145            150            155            160
Ser Val Leu Phe Val Met Ile Leu Pro Thr Val Thr Phe Met Thr Thr
          165            170            175
Asp Ser Leu Arg Ala Val Pro Xaa Leu Leu Ser
          180            185

```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

```

Met Thr Glu Ile Arg Leu Glu His Val Ser Tyr Ala Tyr Gly Gln Glu
 1             5             10             15
Arg Ile Leu Glu Asp Ile Asn Leu Gln Val Thr Ser Gly Glu Val Val
      20             25             30
Ser Ile Leu Gly Pro Ser Gly Val Gly Lys Thr Thr Leu Phe Asn Leu
      35             40             45
Ile Ala Gly Ile Leu Glu Val Gln Ser Gly Arg Ile Val Leu Asp Gly
      50             55             60
Glu Glu Asn Pro Lys Gly His Val Ser Tyr Met Leu Gln Lys Asp Leu
      65             70             75             80
Leu Leu Glu His Lys Thr Val Leu Gly Asn Ile Ile Leu Pro Leu Leu
      85             90             95
Ile Gln Lys Val Asp Lys Ala Glu Ala Ile Ser Arg Ala Asp Lys Ile
      100            105            110
Leu Ala Thr Phe Gln Leu Thr Ala Val Arg Asp Lys Tyr Pro His Glu
      115            120            125
Leu Ser Gly Gly Met Arg Gln Arg Val Ala Leu Leu Arg Thr Tyr Leu
      130            135            140
Phe Gly His Lys Leu Phe Leu Leu Asp Glu Ala Phe Ser Ala Leu Asp
      145            150            155            160
Glu Met Thr Lys Met Glu Leu His Ala Trp Tyr Leu Glu Ile His Lys
      165            170            175
Gln Leu Gln Leu Thr Thr Leu Ile Xaa Thr His Ser Ile Glu Glu Ala
      180            185            190
Leu Xaa Leu Ser Asp Arg Ile Tyr Ile Leu Xaa Asn Xaa Pro Gly Gln
      195            200            205
Ile Val Ser Glu Ile Lys Leu Asp Trp Ser Glu Asp Glu Asp Xaa Glu
      210            215            220
Val Xaa Lys Ile Ala Xaa Lys Arg Gln Ile Leu Ala Glu Leu Gly Leu
      225            230            235            240
Asp Lys

```

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

```

Met Glu His Pro Xaa Glu Ala Ala Asp Ile Leu Ile Lys Asn Ala Pro
 1           5           10           15
Glu Leu Lys Glu Lys Arg Asp Phe Val Ile Glu Ser Gln Lys Tyr Leu
          20           25           30
Ser Lys Glu Tyr Ala Ser Asp Lys Glu Lys Trp Gly Gln Phe Asp Ala
      35           40           45
Ala Arg Trp Asn Ala Phe Tyr Lys Trp Asp Lys Glu Asn Gly Ile Leu
      50           55           60
Lys Glu Asp Leu Thr Asp Lys Gly Phe Thr Asn Glu Phe Val Lys
      65           70           75

```

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

```

Met Val Tyr Thr Ser Leu Ser Ser Lys Asp Gly Asn Tyr Pro Tyr Gln
 1           5           10           15
Leu Asn Ile Ala His Leu Tyr Gly Asn Leu Met Asn Thr Tyr Gly Asp
          20           25           30
Asn Gly Asn Ile Leu Met Leu Lys Tyr Val Ala Glu Lys Leu Gly Thr
      35           40           45
His Val Thr Val Asp Ile Val Ser Leu His Asp Asp Phe Asp Glu Asn
      50           55           60
His Tyr Asp Ile Ala Phe Phe Gly Gly Gly Gln Asp Phe Glu Gln Ser
      65           70           75           80
Ile Ile Ala Asp Asp Leu Pro Ala Lys Lys Glu Ser Ile Asp Asn Tyr
          85           90           95
Ile Gln Asn Asp Gly Val Val Leu Ala Ile Cys Gly Gly Phe Gln Leu
          100          105          110
Leu Gly Gln Tyr Tyr Val Glu Ala Ser Gly Lys Arg Ile Glu Gly Leu
          115          120          125

```

Gly Val Met Gly His Tyr Thr Leu Asn Gln Thr Asn Asn Arg Phe Ile
 130 135 140
 Gly Asp Ile Lys Ile His Asn Glu Arg Phe Arg
 145 150 155

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Met His Gln His Ser Pro His Thr Ala Ser Tyr Thr Ser Ser Arg Asp
 1 5 10 15
 Ala Met Ser Lys Tyr Pro Glu Arg Cys Thr Thr Val Gly Leu Arg Leu
 20 25 30
 Asn Glu Glu Ser Asp Phe Glu Leu Tyr Ala Pro Tyr Gly Leu Glu Asp
 35 40 45
 Ile Leu Asn Phe Lys Phe Val Gln Leu Leu Ile Ser
 50 55 60

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met Phe Glu Ile Phe Asn Met Gly Val Gly Leu Met Leu Ala Val Ser
 1 5 10 15
 Pro Glu Asn Val Glu Arg Val Lys Glu Leu Leu Asp Glu Ala Val Tyr
 20 25 30
 Glu Ile Gly Arg Ile Val Lys Lys Glu Asn Glu Ser Val Ile Ile Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```

Met Met Val Lys Lys His Tyr Phe Lys Asp Asn Glu Glu Asp Ser Lys
 1           5           10           15
Met Arg Arg Ile Leu Leu Leu Val Ala Val Leu Leu Met Ile Pro Ser
          20           25           30
Phe Ile Ser Ala Thr Thr Leu Val Arg Glu Thr Leu Lys Lys Glu Ser
          35           40           45
Leu Lys Lys Phe Ile Ser Glu Gln Phe Gln Gly His Asn Ile Leu Lys
 50           55           60
Lys Thr Tyr Ser Lys Lys Thr His Thr Leu Lys Leu Thr Ile Ser Gly
 65           70           75           80
Asn Tyr Leu Thr Glu Glu Glu Leu Asp Met Ile Ser Ser Lys Arg Gly
          85           90           95
Asp Tyr Gly Leu Ser Asp Val Ser Val Gln Val Ser Gln Leu Ser Asp
          100          105          110
Ser Glu Gln Leu Ser Lys Glu Glu Leu Val Glu Tyr Phe Phe Gln Tyr
          115          120          125
Ile Lys Asp Lys Glu Ala Lys Glu Lys Glu Lys Ala Asn Lys Phe Tyr
          130          135          140
Thr Glu Ser Glu Glu Gln
145          150

```

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

```

Met Ser Ile Glu Pro Arg Arg Arg Trp Arg Asn Ser Thr Val Cys Leu
 1             5             10             15
Glu Ala Glu Leu Tyr Gln Glu Ser Leu Val Leu Ile Gly Gly Asp Pro
          20             25             30
Gly Ile Gly Lys Ser Thr Leu Leu Leu Gln Val Ser Thr Gln Leu Ser
          35             40             45
Gln Val Gly Thr Val Leu Tyr Val Ser Gly Glu Glu Ser Ala Gln Gln
          50             55             60
Ile Lys Leu Arg Ala Glu Arg Leu Gly Asp Phe Asp Ser Glu Phe Tyr
65             70             75             80
Leu Tyr Ala Glu Thr Asn Met Gln Ser Val Arg Ala Glu Val Val Ala
          85             90             95
Tyr Pro Ala Arg Leu Ser His Tyr
          100

```

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

```

Met Ala Thr Lys Gln Lys Glu Val Thr Thr Phe Asp Val Gln Val Ala
 1             5             10             15
Glu Phe Ile Arg Asn His Lys Gln Lys Gly Thr Ala Thr Asp Asp Glu
          20             25             30
Ile Asn Ala Ser Leu Val Ile Pro Phe Thr Leu Asp Ala Asp Gly Ile
          35             40             45
Glu Asp Leu Leu Gln Arg Ile Gln Asp Ala Gly Ile Ser Ile Thr Asp
          50             55             60
Asn Glu Gly Asn Pro Ser Ala Arg Val Leu Ser Asn Glu Glu Glu Pro
65             70             75             80
Glu Leu Ser Asp Glu Asp Leu Ile Gly Ser Thr Ser Ala Lys Val Asn
          85             90             95
Asp Pro Val Arg Met Tyr Leu Lys Glu Ile Gly Val Val Pro Leu Leu
          100             105             110

```

Thr Asn Glu Glu Glu Lys Glu Leu Ala Leu Ala Val Glu Ala Gly Asp
 115 120 125
 Ile Glu Ala Lys Gln Arg Leu Ala Glu Ala Asn Leu Arg Leu Val Val
 130 135 140
 Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Xaa Gln Ser Leu Thr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Met Met Leu Lys Pro Ser Ile Asp Thr Leu Leu Asp Lys Val Pro Ser
 1 5 10 15
 Lys Tyr Ser Leu Val Ile Leu Glu Ala Lys Arg Ala His Glu Leu Glu
 20 25 30
 Ala Gly Ala Pro Ala Thr Gln Gly Phe Lys Ser Glu Lys Ser Thr Leu
 35 40 45
 Arg Ala Leu Glu Glu Ile Glu Ser Gly Asn Val Thr Ile His Pro Asp
 50 55 60
 Pro Glu Gly Lys Arg Glu Ala Val Arg Arg Arg Ile Glu Glu Glu Lys
 65 70 75 80
 Arg Arg Lys Glu Glu Glu Lys Lys Ile Lys Glu Gln Ile Ala Lys
 85 90 95
 Glu Lys Glu Asp Gly Glu Lys Ile
 100

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

```

Met Ile Arg Gln Gly Gln Met Leu Glu Tyr Ala Glu Tyr Val Gly Asn
 1             5             10             15
Tyr Tyr Gly Thr Pro Leu Thr Tyr Val Asn Glu Thr Leu Asp Lys Gly
          20             25             30
Ile Asp Val Phe Leu Glu Ile Glu Val Gln Gly Ala Leu Gln Val Lys
      35             40             45
Lys Lys Val Pro Asp Ala Val Phe Ile Phe Leu Thr Pro Pro Asp Leu
 50             55             60
Asp Glu Leu Gln Glu Arg Leu Val Gly Arg Gly Thr Asp Ser Ala Glu
65             70             75             80
Val Ile Ala Gln Arg Ile Glu Lys Ala Lys Glu Glu Ile Ala Leu Met
          85             90             95
Arg Glu Tyr Asp Tyr Ala Ile Val Asn Asp Gln Val Pro Leu Ala Ala
      100             105             110
Glu Arg Val Lys Cys Val Ile Glu Ala Glu His Phe Cys Val Asp Arg
      115             120             125
Val Ile Gly His Tyr Gln Glu Met Leu Pro Lys Ser Pro Thr Thr Arg
      130             135             140

```

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```

Met Ser Arg Leu Leu Val Ile Gly Cys Gly Gly Val Ala Gln Val Ala
 1             5             10             15
Ile Ser Lys Ile Cys Gln Asp Ser Glu Thr Phe Thr Glu Ile Met Ile
          20             25             30
Ala Ser Arg Thr Lys Ser Lys Cys Asp Asp Leu Lys Ala Lys Leu Glu
      35             40             45
Gly Lys Thr Ser Thr Lys Ile Glu Thr Ala Ala Leu Asp Ala Asp Lys
      50             55             60
Val Glu Glu Val Ile Ala Leu Ile Glu Ser Leu Gln Thr Ser Lys Leu
      65             70             75             80
Phe

```

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

```

Met His Glu Ser Phe His Val Asp Asp Pro Thr Leu Tyr Ser Arg Glu
 1             5             10             15
Trp Phe Ser Trp Ala Asn Met Met Phe Cys Glu Leu Val Leu Asp Tyr
          20             25             30
Leu Asp Ile Arg
          35

```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

```

Met Arg Phe Tyr Phe Met Glu Asn Val Val Val His Ile Ile Ser His
 1             5             10             15
Ser His Trp Asp Arg Glu Trp Tyr Leu Pro Phe Glu Ser His Arg Met
          20             25             30
Gln Leu Val Glu Leu Phe Asp Asn Leu Phe Asp Leu Phe Glu Asn Asp
          35             40             45
Pro Glu Phe Lys Ser Phe His Leu Asp Gly Gln Thr Ile Val Leu Asp
          50             55             60
Asp
65

```

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

```

Met Leu Leu Tyr Ile Leu Ser His Ile Ala Thr Gly Ile Val Ser Gly
 1             5             10             15
Thr Cys Leu Leu Lys Ala Ile Val Cys Asn Trp Trp Asn Cys Leu Thr
      20             25             30
Ile Ser Leu Ile Ser Leu Lys Met Thr Leu Ser Ser Arg Val Ser Thr
      35             40             45
Trp Met Asp Lys Leu Leu Ser Leu Thr Thr Asn Leu Gln Ile Arg Pro
      50             55             60
Glu Asn Arg Asp Lys Val Gln Arg Tyr Ile Asp Glu Gly Lys Leu Lys
65             70             75             80
Ile Gly Pro Phe Tyr Ile Leu Gln Asp Asp Tyr Leu Ile Ser Ser Glu
      85             90             95
Ala Asn Val Arg Asn Thr Leu Ile Gly Gln Gln Glu Ala Ala Lys Trp
      100            105            110
Gly Lys Ser Thr Gln Ile Gly Tyr Phe Pro Asp Thr Phe Gly Asn Met
      115            120            125
Gly Gln Ala Pro Gln Ile Leu Gln Lys Ser Gly Ile His Val Ala Ala
      130            135            140
Phe Gly Arg Gly Val Lys Pro Ile Gly Phe Asp Asn Gln Val Leu Glu
145            150            155            160
Asp Glu Gln Phe Thr Ser Gln Phe Ser Glu Met Tyr Trp Gln Gly Val
      165            170            175
Asp Gly Ser Arg Val Leu Gly Ile Leu Phe Ala Asn Trp Tyr Ser Asn
      180            185            190
Gly Asn Glu Ile Pro Val Asp Lys Asp Glu Ala Leu Thr Phe Trp Lys
      195            200            205
Gln Lys Leu Ser Asp Val Arg Cys Leu Arg Phe Asp Gln Pro Met Val
      210            215            220
Asp Asp Glu Thr Ala Val Asn Thr Ser Leu Ser Gln Lys Lys Ser Glu
225            230            235            240
Arg Ser His Ser Val Trp Gln Met Asn Ser Ser Arg Met
      245            250

```

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```

Met Thr Ile Val Gly Cys Arg Ile Asp Gly Arg Leu Ile His Gly Gln
 1           5           10           15
Val Ala Asn Leu Trp Ala Gly Lys Leu Asn Val Ser Arg Ile Met Val
          20           25           30
Val Asp Asp Glu Val Val Asn Asn Asp Ile Glu Lys Ser Gly Leu Lys
          35           40           45
Leu Ala Thr Pro Pro Gly Val Lys Leu Ser Ile Leu Pro Val Glu Lys
          50           55           60
Ala Ala Ala Asn Ile Leu Ala Gly Lys Tyr Asp Ser Gln Arg Leu Phe
65           70           75           80
Ile Val Ala Arg Lys Pro Asp Arg Phe Pro Trp Phe Gly Arg Ser Arg
          85           90           95
Cys Thr Thr

```

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```

Met Ile Gln His Pro Arg Ile Gly Ile Arg Pro Thr Ile Asp Gly Arg
 1           5           10           15
Arg Gln Gly Val Arg Glu Ser Leu Glu Val Gln Thr Met Asn Met Ala
          20           25           30

```

```

Lys Ser Val Ala Asp Leu Ile Ser Ser Thr Leu Lys Tyr Pro Asp Gly
  35                      40                      45
Glu Pro Val Glu Cys Val Ile Ser Pro Ser Thr Ile Gly Arg Val Pro
  50                      55                      60
Glu Ala Ala Ala Ser His Glu Leu Phe Lys Lys Ser Asn Val Cys Ala
  65                      70                      75                      80
Thr Ile Thr Val Thr Pro Cys Trp Cys Tyr Gly Ser Glu Thr Met Asp
                      85                      90                      95
Met Ser Pro Asp Ile Pro His Ala Ile Trp Gly Phe Asn Gly Thr Glu
                      100                      105                      110
Arg Pro Gly Ala Val Tyr Leu Ala Ala Val Leu Ala Ser His Ala Gln
                      115                      120                      125
Lys Gly Ile Pro Ala Phe Gly Ile Tyr Gly Arg Asp Val Gln Glu Ala
                      130                      135                      140
Asn Asp Thr Asp Ile Pro Glu Asp Val Lys Glu Asn Phe
145                      150                      155

```

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```

Met Leu Leu Ser Thr Lys Gly Ile Glu Glu Gln Glu Ile Ala Arg Pro
  1                      5                      10                      15
Thr Leu Glu Arg Leu Phe Ser Met Arg Glu Asn Tyr Lys Val Thr Gly
                      20                      25                      30
Arg His Pro Gly Tyr Arg Lys Tyr Asn Gly Asp Gly Ser Met Lys Glu
                      35                      40                      45
Thr Glu Lys
  50

```

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Thr | Leu | Thr | Pro | Asp | Val | Ile | Tyr | Gln | Glu | Pro | Asp | Ile | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Tyr | Gln | His | Glu | Asp | Phe | Ser | Leu | Val | Lys | Ile | Arg | Gln | Ile | Arg | Phe |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Cys | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Val | Val | Gly | Leu | Met | Gly | Asn | Ile | Gly | Gln | Ala | Asn | Tyr |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ala | Ala | Ser | Lys | Ala | Gly | Leu | Ile | Gly | Phe | Thr | Lys | Ser | Val | Ala | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Val | Ala | Ser | Arg | Asn | Ile | Arg | Val | Asn | Val | Ile | Ala | Pro | Gly | Asn |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Asp | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

```

Met Lys Leu Glu His Lys Asn Ile Phe Ile Thr Gly Ser Ser Arg Gly
 1             5             10             15
Ile Gly Leu Ala Ile Ala His Lys Phe Ala Gln Ala Gly Ala Asn Ile
          20             25             30
Val Leu Asn Ser Arg Gly Ala Ile Ser Glu Glu Leu Leu Ala Glu Phe
          35             40             45
Ser Asn Tyr Gly Ile Lys Val Val Pro Ile Ser Gly Asp Val Ser Asp
          50             55             60
Phe Ala Asp Ala Lys Arg Met Ile Asp Gln Ala Ile Ala Glu Leu Gly
65             70             75             80
Ser Val Asp Val Leu Val Asn Asn Ala Gly Ile Thr Gln Asp Thr Leu
          85             90             95
Met Leu Lys Met Thr Glu Ala Asp Phe Glu Lys Val Leu Lys Val Asn
          100            105            110
Leu Thr Gly Ala Phe Asn Met Thr Gln Ser Val Phe Gly Asn Arg
          115            120            125

```

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

```

Met Glu Ser Met Pro Arg Ile Gly Leu Leu Val Thr Val Glu Asn Arg
 1             5             10             15
Asp Thr Glu Thr Ile Phe Asn Ala Ala Gly Leu Asp Phe Asp Val Leu
          20             25             30
Lys Ala Ser Ala Ile Ala Tyr Ile Asn Ala Asn Thr Phe Val Gln Lys
          35             40             45
Glu Asn Ala Gly Glu Met Gly Arg Ser Val Ser Tyr His Asp Met Arg
          50             55             60
Ser Val
65

```

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```

Met Arg Gln Gly Gln Gly Ser Val Glu Ala Ile Phe Asn Ala Ile Asp
 1             5             10             15
Lys Phe Phe Asn Gln Ser Val Arg Leu Val Ser Tyr Thr Ile Asn Ala
             20             25             30
Val Thr Asp Gly Ile Asp Ala Gln Asp Arg Val Val Gly His Cys
          35             40             45

```

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

Met Val Glu Asn Pro Glu Gly Phe His Phe Asp Asp Leu Gln Leu Gln
 1             5             10             15
Thr His Ala Asp Asn Asp Ile Glu Ala Leu Val Ser Leu Ala Asn Met
             20             25             30
Asp Gly Glu Lys Val Glu Phe Asn Ala Thr Gly Thr Gly Phe Arg
          35             40             45

```

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```

Met Asn Phe Gln Leu Ala Lys Tyr Ser Leu Leu Lys Lys Phe Ser Glu
 1             5             10             15
Asn Ile Gly Phe Thr Thr Pro Glu Glu Cys Gly Ala Ile Phe Gln Tyr
      20             25             30
Leu Ile Glu Asn Val Gln Thr Asp Arg Gln Ile Ile Tyr Ser Pro Pro
      35             40             45
Cys His Asp Glu Leu Arg Met Ala Val Ala Asn Ser Leu Ala Ala Val
      50             55             60
Lys Asn Gly Ala Gly Leu Phe Glu Glu Thr Ile His Gly Ile Arg Glu
      65             70             75             80
Arg Ala Glu Asn Ala Ala Leu Glu Glu Ile Ala Val Ala Leu Asn Ile
      85             90             95
Arg Gln Asp Tyr Tyr Gln Val Glu Thr Ser Ile Val Leu Asn Glu Thr
      100            105            110
Ile Asn Thr Ser Glu Met Val Ser Arg Phe Ser Gly Ile Pro Val Pro
      115            120            125
Lys Asn Lys Ala Val Val Gly Gly Asn Thr Phe Ser His Glu Ser Gly
      130            135            140
Ile His Gln Asp Gly Val Leu Lys Asn Pro Leu Thr Tyr Glu Ile Ile
      145            150            155            160
Thr Pro Glu Leu Val Gly Val Lys Ile Pro Leu Gly Lys Leu Ser Gly
      165            170            175
Arg His Ala Phe Val Glu Lys Leu Arg Glu Leu Ala Leu Asp Phe Thr
      180            185            190
Glu Glu Asp Ile Lys Pro Phe Phe Ala Lys Phe Lys Ala Leu Ala Asp
      195            200            205
Lys Lys
      210

```

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

```

Met Ser Gln Gln Val Lys Asn Ala His Asn Leu Tyr Ile His Ala Ile
 1             5             10             15
Gln Asp Gly Arg Val Ala Glu Ala Gln Ala Gln Ser Val Gly Asp Thr
      20             25             30
Tyr Ile Gln His Ser Thr Gly Val Pro Asp Gly Lys Glu Gly Phe Ala
      35             40             45
Ala Phe Phe Ala Asp Phe Phe Glu Arg His Pro Glu Arg Gln Ile Lys
      50             55             60
Ile Val Arg Thr Ile Glu Asp Gly Asn Leu Val Phe Val His Val Pro
65             70             75             80
Ser Ile Ser Glu Trp Trp Arg Ser Ser Met Gly Asp Asp Gly Tyr Phe
      85             90             95
Pro Cys Gly

```

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```

Met Glu Met Gln Thr Ser Ala Gln Leu Leu Thr Asn Lys Ile Phe Leu
 1             5             10             15
Lys Asn Pro Leu Lys Ala Leu Val Glu Glu Lys Tyr Gly Ile Glu Tyr
      20             25             30
Glu Glu Phe Thr Asn Pro Trp His Ala Ala Ile Ser Ser Phe Val Ala
      35             40             45
Phe Phe Leu Arg Ser Leu Pro Pro Met Leu Ser Val Thr Ile Phe Pro
      50             55             60
Ser Glu Tyr Arg Ile Pro Ala Thr Val Leu Ile Val Gly Val Ala Leu
65             70             75             80
Leu Leu Thr Gly Tyr Thr Ser Ala Arg Leu Gly Lys Asp Pro Thr Arg
      85             90             95
Thr Ala Met Ile Arg Asn Leu Ala Ile Gly Leu Leu Thr Met Gly Val
      100             105             110
Thr Phe Leu Leu Glu Gln Leu Phe Ser Ile
      115             120

```

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

Met Ala Phe Phe Leu Cys Pro His Phe Arg Ser Asn His Trp Lys Ile
  1             5             10             15
Leu Thr Val Ser Asp Thr Met Glu Glu Lys Arg Leu Glu Tyr Pro Met
      20             25             30
Val Thr Phe Leu Gly Asn Pro Val Ser Phe Thr Gly Lys Gln Leu Gln
      35             40             45
Val Gly Asp Lys Ala Leu Asp Phe Ser Leu Thr Thr Thr Asp Leu Ser
      50             55             60
Lys Lys Ser Leu Ala Asp Phe Asp Gly Lys Lys Lys Val Leu Ser Val
      65             70             75             80
Val Pro Ser Ile Asp Thr Gly Ile Cys Ser Thr Gln Thr Arg Arg Phe
      85             90             95
Asn Glu Glu Leu Ala Gly Leu Asp Asn Thr Val Val Leu Thr Val Ser
      100            105            110
Met Asp Leu Pro Phe Ala Gln Lys Arg Trp Cys Gly Ala Glu Gly Leu
      115            120            125
Asp Asn Ala Ile Met Leu Ser Asp Tyr Phe Asp His Ser Phe Gly Arg
      130            135            140
Asp Tyr Ala Leu Leu Ile Asn Glu Trp His Leu Leu Ala Arg Ala Val
      145            150            155            160
Phe Val Leu Asp Thr Asp Asn Thr Ile Arg Tyr Val Glu Tyr Val Asp
      165            170            175
Asn Ile Asn Ser Glu Pro Asn Phe Glu Ala Ala Ile Ala Ala Ala Lys
      180            185            190
Ala Leu

```

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

Met Gly Tyr Arg Pro Ser Thr Ala Asn Ala Ile Ile His Gln Val Arg
 1             5             10             15
Glu Leu Leu Val Ser Arg Gly Tyr Thr Phe Tyr Asn Arg Lys Arg Leu
      20             25             30
Met Val Val Pro Lys Ser Val Val Lys Glu Leu Leu Gly Met Glu Leu
 35             40             45
  
```

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

Met Gln Ala Val Glu His Phe Ile Lys Gln Phe Val Pro Glu His Tyr
 1             5             10             15
Asp Leu Phe Leu Asp Leu Ser Arg Glu Thr Lys Thr Phe Ser Gly Lys
      20             25             30
Val Thr Ile Thr Gly Gln Ala Gln Ser Asp Arg Ile Ser Leu His Gln
 35             40             45
Lys Asp Leu Glu Ile Thr Ser Val Glu Val Ala Gly Gln Ala Arg Pro
 50             55             60
Phe Thr Val Asp His Asp Asn Glu Ala Leu His Ile Glu Leu Ala Glu
65             70             75             80
Ala Gly Gln Val Glu Leu Val Leu Ala Phe Ser Gly Lys Ile Thr Asp
      85             90             95
Asn Met Thr Gly Ile Tyr Pro Ser Tyr Tyr Thr Val Asp Gly Val Lys
 100            105            110
Lys Glu Val Leu Ser Thr Gln Phe Glu Ser His Phe Ala Arg Glu Ala
 115            120            125
  
```

```

Phe Pro Cys Val Asp Glu Pro Glu Ala Lys Ala Thr Phe Asp Leu Ser
130                135                140
Leu Arg Phe Asp Gln Ala Glu Gly Glu Leu Ala Leu Ser Asn Met Pro
145                150                155                160
Glu Ile Asp Val Glu Asn Arg Lys Glu Thr Gly Ile Trp Lys Phe Glu
                165                170                175
Thr Thr Pro Arg Met Ser Ser Tyr Leu Leu Ala Phe Val Ala Gly Asp
                180                185                190
Leu Gln Gly Val Thr Ala Lys Thr Lys Asn Gly Thr Leu Val Gly Cys
                195                200                205
Leu Leu Asn Gln Ser Thr Ser Thr Phe Lys Ser
                210                215

```

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

```

Met Ser Gln Glu Phe Leu Ala Arg Ile Leu Glu Gln Lys Ala Arg Glu
1          5          10          15
Val Glu Gln Met Lys Leu Glu Gln Ile Gln Pro Leu Arg Gln Thr Tyr
                20          25          30
Arg Leu Ala Glu Phe Leu Lys Asn His Gln Asp Arg Leu Gln Val Ile
                35          40          45
Ala Glu Val Lys Lys Ala Ser Pro Ser Phe Gly Glu Ile Ser Ile Ser
                50          55          60
Met Trp Ile Leu Cys Asn Arg Pro Arg Leu Met Lys Lys Thr Glu Gln
65          70          75          80

```

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

```

Met Ser Ser Phe Thr Pro Glu Asp Leu Gly Met Glu Gly Tyr Ala Met
 1             5             10             15
Glu Asp Ile Arg Gly Gly Asn Ala Gln Glu Asn Ala Glu Ile Leu Leu
      20             25             30
Ser Val Leu Lys Asn Glu Ala Ser Pro Phe Leu Glu Thr Thr Val Leu
      35             40             45
Asn Ala Gly Leu Gly Phe Tyr Ala Asn Gly Lys Ile Asp Ser Ile Lys
      50             55             60
Glu Gly Val Ala Leu Ala Arg Gln Val Ile Ala Arg Gly Lys Ala Leu
      65             70             75             80
Glu Lys Leu Arg Leu Leu Gln Glu Tyr Gln Lys
      85             90

```

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

```

Met Ile Tyr Thr Val Thr Leu Asn Pro Ser Ile Asp Tyr Ile Val Arg
 1             5             10             15
Leu Asp Gln Val Lys Val Gly Ser Val Asn Arg Met Asp Ser Asp Asp
      20             25             30
Lys Phe Ala Gly Gly Lys Gly Ile Asn Val Ser Arg Val Leu Lys Arg
      35             40             45
Leu Asn Ile Ser Asn Thr Ala Thr Gly Phe Ile Gly Gly Phe Thr Gly
      50             55             60
Lys Phe Xaa Xaa Asp Thr Leu Ala Glu Glu Glu Ile Glu Xaa Arg Phe
      65             70             75             80
Val Gln Val Ala Glu Asp Thr Arg Ile Asn Val Lys Ile Xaa Ala Asp
      85             90             95
Gln Glu Thr Glu Ile Asn Gly Thr Gly Pro Thr Val Glu Pro Val Lys
      100             105             110

```

Leu Glu Glu Leu Lys Ala Ile Leu Ser Ser Leu Thr Ala Glu Asp Thr
 115 120 125
 Val Val Phe Ala Gly Ser Ser Ala Lys Asn Leu Gly Asn Val Ile Tyr
 130 135 140
 Lys Gly Phe Asn Leu Leu Asp Ala Pro Asp Trp Cys Ala Ser Gly Leu
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Met Met Gln Val Tyr Phe Asp Gln Gly Ile Tyr Asn Lys Lys Ala Val
 1 5 10 15
 Phe Glu Val Tyr Phe Arg Gln Gln Pro Phe Lys Asn Gly Tyr Ala Val
 20 25 30
 Phe Ala Gly Leu Glu Arg Ile Val Asn Tyr Leu Glu Asp Leu Arg Phe
 35 40 45
 Ser Asp Ser Asp Ile Ala Tyr Leu Glu Ser Leu Gly Tyr His Gly Ala
 50 55 60
 Phe Leu Asp Tyr Leu Arg Asn Phe Lys Leu Glu Leu Thr Val Arg Ser
 65 70 75 80
 Ala Gln Glu Gly Asp Leu Val Phe Ala Asn Glu Pro Ile Val Gln Val
 85 90 95
 Glu Gly Pro Leu Ala Gln Cys Gln Leu Val Glu Thr Ala Leu Leu Asn
 100 105 110
 Ile Val Asn Tyr Gln Thr Leu Val Ala Thr Lys Ala Ala Pro Tyr Pro
 115 120 125
 Phe Gly Tyr Arg Lys
 130

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```

Met Lys Ile Ile Ile Gln Arg Val Lys Lys Ala Gln Val Ser Ile Glu
 1             5             10             15
Gly Gln Ile Gln Gly Lys Ile Asn Gln Gly Leu Leu Leu Leu Val Gly
          20             25             30
Val Gly Pro Glu Asp Gln Glu Glu Asp Leu Asp Tyr Ala Val Arg Lys
          35             40             45
Leu Val Asn Met Arg Ile Phe Ser Asp Val Glu Gly Lys Met Asn Leu
          50             55             60
Ser Val Lys Asp Ile Glu Gly Glu Ile Leu Ser Ile Leu Ser Leu Pro
          65             70             75             80
Leu Cys Gly Tyr

```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

Met Ile Lys Gly Thr Ile Lys Thr Val Ser Ile Met Ala Ala Thr Ser
 1             5             10             15
Gly Phe Leu Leu Tyr Asn Glu Val Phe Phe Leu Thr Asn Gly Ala Ala
          20             25             30
Gly Thr Lys Ser Ile Ser Phe Val Ile Arg Glu Leu Ala Val Ala Ser
          35             40             45
Ser Arg Thr Gln Tyr Ala Arg Ala Asn Thr Ile Gly Val Ile Gln Ile
          50             55             60
Leu Gly Gly Met Leu Ile Ile Val Cys Ile Asn Ile Leu Phe Arg Glu
          65             70             75             80
Arg Lys Arg Leu Lys Gly Gly Lys
          85

```

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```

Met Gly Phe Gly Ile Pro Ala Ala Ile Gly Ala Lys Ile Ala Asn Pro
 1           5           10           15
Asp Lys Glu Val Val Leu Phe Val Gly Asp Gly Gly Phe Gln Met Thr
          20           25           30
Asn Gln Glu Leu Ala Ile Leu Asn Ile Tyr Lys Val Pro Ile Lys Val
          35           40           45
Val Met Leu Asn Asn His Ser Leu Gly Met Val Arg Gln Trp Gln Glu
          50           55           60
Ser Phe Tyr Glu Gly Arg Thr Ser Glu Ser Val Phe Asp Thr Leu Pro
65           70           75           80
Asp Phe Gln Leu Met Ala Gln Ala Tyr Gly Ile Lys Asn Tyr Lys Phe
          85           90           95
Asp Asn Pro Glu Thr Leu Ala Gln Asp Leu Glu Ala Thr Thr Glu Asp
          100          105          110
Val Pro Met Leu Ile Glu Val Asp Ile Ser Arg Lys Glu Gln Val Leu
          115          120          125
Pro Met Val Pro Ala Gly Lys Ser Asn His Glu Met Leu Gly Val Lys
          130          135          140
Phe His Ala
145

```

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

```

Met Trp Leu Pro Leu Asp Arg Asn Asn Lys Gly Gln Asn Ile Ala Gly
 1             5             10             15
Ala Arg Gln Ala Ala Glu Gly Ile Phe Gly Val Asp Ala Ser Gln Leu
          20             25             30
Thr Val Pro Gln Ala Ala Phe Leu Ala Gly Leu Pro Gln Ser Pro Ile
          35             40             45
Thr Tyr Ser Pro Tyr Glu Asn Thr Gly Glu Leu Lys Asn
          50             55             60

```

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

```

Met Tyr Leu Gly Asp Leu Met Glu Lys Ala Glu Cys Gly Gln Phe Ser
 1             5             10             15
Ile Leu Ser Phe Leu Leu Gln Glu Ser Gln Thr Thr Val Lys Ala Val
          20             25             30
Met Glu Glu Thr Gly Phe Ser Lys Ala Thr Leu Thr Lys Tyr Val Thr
          35             40             45
Leu Leu Asn Asp Lys Ala Leu Asp Ser Gly Leu Glu Leu Thr Ile His
          50             55             60
Ser Glu Asp Glu Asn Leu Arg Leu Ser Ile Gly Ala Ala Thr Lys Gly
          65             70             75             80
Arg Asp Ile Pro Glu Leu Val Phe Trp Ile Val Leu Leu Asn Thr Arg
          85             90             95
Phe Trp Phe Ile Phe Ser Thr Thr Asn Ser Phe
          100             105

```

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

```

Met Lys Glu Ile Ile Glu Lys Leu Ala Lys Phe Glu Asn Leu Ser Gly
 1             5             10             15
Val Glu Met Thr Asp Val Ile Glu Arg Ile Val Thr Gly Arg Val Thr
      20             25             30
Glu Ala Gln Ile Ala Ser Leu Leu Leu Ala Leu Lys Met Lys Gly Glu
      35             40             45
Thr Pro Glu Glu Arg Thr Ala Ile Ala Gln Val Met Arg Gly His Ala
      50             55             60
Gln His Ile Pro Thr Glu Ile His Asp Ala Met Asp Asn Cys Gly Thr
      65             70             75             80
Gly Gly Asp Lys Ser Phe Ser Phe Asn Ile Ser Thr Thr Ala Ala Phe
      85             90             95
Val Leu Ala Gly Gly Gly Ile His Met Ala Lys His Gly Asn Arg Ser
      100             105             110
Ile Ser Ser Lys Ser Gly Ser Ala Asp Ser Xaa Asn Leu Gly Asn Gln
      115             120             125
Ser

```

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

```

Met Asn Val Gln Met Ser Ser Lys Thr Asn Ile Leu Arg Ala His Ala
 1             5             10             15
Glu Met Gln Asn Ile Gln Arg Arg Ala Asn Glu Glu Arg Gln Asn Leu
      20             25             30
Gln Arg Tyr Arg Ser Gln Asp Leu Ala Lys Ala Ile Leu Pro Ser Leu
      35             40             45
Asp Asn Leu Glu Arg Ala Leu Ala Val Glu Gly Leu Thr Asp Asp Val
      50             55             60

```

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Gly | Leu | Gly | Met | Val | Gln | Glu | Ser | Leu | Ile | His | Ala | Leu | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Glu | Glu | Gly | Ile | Glu | Glu | Ile | Ala | Ala | Asp | Gly | Glu | Phe | Asp | His | Asn |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Tyr | His | Met | Ala | Ile | Gln | Thr | Leu | Pro | Ala | Asp | Asp | Asp | His | Pro | Val |
| | | | 100 | | | | | | 105 | | | | | 110 | |
| Asp | Thr | Ile | Ala | Gln | Val | Phe | Gln | Lys | Gly | Tyr | Lys | Leu | His | Asp | Arg |
| | | | 115 | | | | | 120 | | | | | 125 | | |
| Ile | Leu | Arg | Pro | Ala | Met | Val | Val | Val | Tyr | Asn | | | | | |
| | | | 130 | | | | | 135 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```

Met Ser Asn Lys Ser Tyr Ser Lys Phe Gln Glu Glu Val Ser Leu Lys
 1           5           10           15
Tyr Gly Phe Ile Gly Leu Lys Leu Asp Lys Leu Ser Leu Thr Ala Glu
          20          25          30
Val Ser Glu Glu Phe His Ser Glu Ile Leu Ser Gly Asn Phe Thr Leu
          35          40          45
Tyr Asp Ile Ser Val
          50

```

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

```

Met His Phe Asp Lys Ser Lys Phe Gly Ala Val Phe Ser Ala Pro Gly
 1             5             10             15
Leu Tyr Glu Val Glu Val Ile Asn Asn Ala Ser Phe Gly Gln Asn Ala
      20             25             30
Gln Tyr Glu Val Ile Gln Ser Arg Lys Leu Gly Thr Phe Ala Glu Leu
      35             40             45
Ile Glu Met Ala Lys Ile Lys
      50             55

```

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

```

Met Ile Gln Ala Val Phe Glu Arg Ala Glu Asp Gly Glu Leu Arg Ser
 1             5             10             15
Ala Glu Ile Thr Gly His Ala Glu Ser Gly Glu Tyr Gly Leu Asp Val
      20             25             30
Val Cys Ala Ser Val Ser Thr Leu Ala Ile Asn Phe Ile Asn Ser Ile
      35             40             45
Glu Lys Phe Ala Gly Tyr Glu Pro Ile Leu Glu Leu Asn Glu Asp Glu
      50             55             60
Gly Gly Tyr Leu Met Val Glu Ile Pro Lys Asp Leu Pro Ser His Gln
      65             70             75             80
Arg Glu Met Thr Gln Leu Phe Phe Glu Ser Phe Phe Leu Gly Met Ala
      85             90             95
Asn Leu Ser Glu Asn Ser Ser Glu Phe Val Gln Thr Arg Val Ile Thr
      100            105            110
Glu Asn

```

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

```

Met Thr Ala Ile Ser Met Lys Trp Leu Asn Asp Tyr Ile Trp Pro Ala
 1             5             10             15
Glu Ser Glu Phe Thr Pro Asp Met Thr Thr Asn Ala Val Lys Glu Ala
          20             25             30
Leu Thr Glu Met Leu Gln Ser Gly Thr Thr Thr Phe Asn Asp Met Tyr
          35             40             45
Asn Pro Asn Gly Val Asp Ile Gln Gln Ile Tyr Gln Val Val Lys Thr
          50             55             60
Ser Lys Met Arg Cys Tyr Phe Ser Pro Thr Leu Phe Ser Ser Glu Thr
          65             70             75             80
Glu Thr Thr Ala Glu Thr Ile Ser Arg Thr Arg Ser Ile Ile Asp Glu
          85             90             95
Ile Leu Lys Tyr Lys Asn Pro Lys Phe Gln Gly Leu Trp
          100             105

```

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

```

Met Val Arg Glu Ser Ala Glu Ser Ala Gly Phe Phe Leu Glu Thr His
 1             5             10             15
Met Val Gln Gly Glu Trp Asn Thr Cys Val Phe Lys Lys Thr Lys Asp
          20             25             30
Ile Ser Gly Val Ile Gly Gly
          35

```

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```

Met Thr Val Asp Arg Glu Gly Phe Glu Ala Ala Met Lys Glu Gln Gln
 1           5           10           15
Glu Arg Ala Arg Ala Ser Ala Val Lys Gly Gly Ser Met Gly Met Gln
           20           25           30
Asn Gly Asn Ser Ser Lys His His Cys Arg Lys Cys Leu Gln Leu Gln
          35           40           45
Cys
  
```

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

```

Met Lys Ala Gln Leu Val Pro Ser Arg Ser Lys Tyr Leu Ile Asn Asp
 1           5           10           15
Asn Thr Val Val Leu Phe Phe Gly Thr Arg Thr Asp Tyr Thr Arg Lys
           20           25           30
Tyr Asp Leu Asp Leu Val Arg Glu Val Ala Gly Asp Gln Ile Ala Arg
          35           40           45
Arg Val Val Leu Leu Ser Asp Gln Ala Phe Gly Leu Glu Asn Val Lys
          50           55           60
Glu Val Ala Leu Gly Cys Gly Gly Val Leu Asn Asp Ile Tyr Arg Val
          65           70           75           80
Phe Pro Tyr Ile Val Tyr Ala Gln Leu Phe Ala Leu Leu Thr Ser Leu
           85           90           95
Lys Val Glu Asn Lys Pro Asp Thr Pro Ser Pro Thr Gly Thr Val Asn
          100          105          110
  
```

Arg Val Val Gln Gly Val Ile Ile His Glu Tyr Gln Lys
 115 120 125

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Met Ala Val Asn Asn Glu Ile Gly Ser Ile Gln Xaa Ile Glu Ala Ile
 1 5 10 15
 Ser Glu Phe Leu Ala Asp Lys Pro Thr Ile Ser Phe His Val Asp Ala
 20 25 30
 Val Gln Ala Leu Ala Lys Ile Pro Thr Glu Lys Tyr Leu Thr Glu Arg
 35 40 45
 Val Asp Cys Ala Thr Phe Ser Ser His Lys Phe His Gly Val Arg Gly
 50 55 60
 Val Gly Phe Val Tyr Ile Lys Ser Gly Lys Lys Ile Thr Pro Leu Leu
 65 70 75 80
 Thr Gly Gly Gly Gln Glu Arg Asp Tyr Arg Ser Thr Thr Glu Asn Val
 85 90 95
 Ala Gly Ile Ala Ala Thr Ala Lys Ala Leu Arg Leu Ser Met Glu Lys
 100 105 110
 Leu Asp Ile Phe Arg Ser Lys Thr Gly Gln Met Lys Ala Val Ile His
 115 120 125
 Gln Ala Leu Leu Asn Tyr Pro Asp Ile Phe Val Phe Ser Asp Glu Glu
 130 135 140
 Asp Phe Ala Pro His Ile Leu Thr Phe Gly Ile Lys Gly Val Arg Gly
 145 150 155 160
 Glu Val Ile Val His Ala Phe Glu Asp Tyr Asp Ile Phe Ile Ser Thr
 165 170 175
 Thr Ser Ala Cys Ser Ser Lys Ala Gly Lys Pro Ala Gly Thr Leu Ile
 180 185 190
 Ala Met Gly Val Asp Lys Asp Lys Ala Lys Ser Ala Val Arg Leu Ser
 195 200 205
 Leu Asp Leu Glu Asn Asp Met Ser Gln Val Glu Gln Phe Leu Thr Lys
 210 215 220

Leu Lys Leu Ile Tyr Asn Gln Thr Arg Lys Val Arg
 225 230 235

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Met Leu Val Thr Gly Ala Ile Leu Gly Val Asn Val His Ile Phe Ser
 1 5 10 15
 Pro Lys Glu Leu Phe Pro Glu Lys Glu Ile Val Glu Leu Ala Glu Gly
 20 25 30
 Phe Ala Lys Glu Ser Gly Ala His Val Leu Ile Thr Glu Asp Ala Asp
 35 40 45
 Glu Ala Val Lys Asp Ala Asp Val Leu Tyr Thr Asp Val Trp Val Ser
 50 55 60
 Met Gly Glu Glu Asp Lys Phe Ala Glu Arg Val Ala Leu Leu Lys Pro
 65 70 75 80
 Tyr Gln Val Asn Met Asp Leu Val Lys Lys Ala Gly Asn Glu Asn Leu
 85 90 95
 Ile Phe Leu His Cys Leu Pro Ala Phe His Asp Thr His Thr Val Tyr
 100 105 110
 Gly Lys Asp Val Ala Glu Lys Phe Gly Val Glu Glu Met Glu Val Thr
 115 120 125
 Asp Glu Val Phe Arg Ser Lys Tyr Ala Arg His Phe Asp Gln Ala Glu
 130 135 140
 Asn Arg Met His Thr Ile Lys Ala Val Met Ala Ala Thr Leu Gly Asn
 145 150 155 160
 Leu Tyr Ile Pro Lys Val
 165

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

```

Met Arg Leu Glu Gln Asp Cys Pro Val Phe Leu Lys Ile Lys Glu Lys
 1           5           10           15
Asp Met Ala Ser Lys Met Leu His Thr Cys Leu Arg Val Glu Asn Leu
      20           25           30
Glu Lys Ser Ile Ala Phe Tyr Gln Asp Ala Phe Gly Phe Lys Glu Leu
      35           40           45
Arg Arg Arg Asp Phe Pro Asp His Ala Phe Thr Ile Val Tyr Leu Gly
      50           55           60
Leu Glu Gly Asp Asp Tyr Glu Leu Glu Leu Thr Tyr Asn Tyr Asp His
      65           70           75           80
Gly Pro Tyr Val Val Gly Asp Gly Phe Ala His Ile Ala Leu Ser Thr
      85           90           95
Pro Asp Leu Glu Ala Leu His Gln Glu His Ser Thr Lys Gly Tyr Glu
      100          105          110
Val Thr Glu Pro Asn Gly Leu Pro Gly Thr Ala Pro Asn Tyr Tyr Phe
      115          120          125
Val Lys Asp Pro Asp Gly Tyr Lys Val Glu Val Ile Arg Glu Lys
      130          135          140

```

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

```

Met Asp His Thr Ile Phe Cys Val Gly Tyr Arg Val Met Gln Lys Asp
 1           5           10           15
Leu Glu Gly Thr Leu Asp Ala Glu Lys Leu Lys Ala Ala Gly Val Pro
      20           25           30
Phe Gly Pro Leu Phe Gly Lys Ile Lys Asn Gly Gln Asp Leu Val Leu
      35           40           45

```

```

Glu Asp Gly Thr Glu Ile Lys Ala Ala Asp Tyr Ile Ser Ala Pro Arg
 50                      55                      60
Pro Gly Lys Ile Ile Thr Ile Leu Gly Asp Thr Arg Lys Thr Asp Ala
65                      70                      75                      80
Ser Val Arg Leu Ala Val Asn Ala Asp Val Leu Val His Glu Ser Thr
                      85                      90                      95
Tyr Gly Lys Gly Asp Glu Lys Ile Ala Arg Asn His Gly His Ser Thr
                      100                     105                     110
Asn Met Gln Ala Ala Gln Val Ala Val Glu Ala Gly Ala Lys Arg Leu
                      115                     120                     125
Leu Leu Asn His Ile Ser Ala Arg Phe Leu Ser Lys Asp Ile Ser Lys
                      130                     135                     140
Leu Lys Lys Asp Ala Ala Thr Ile Phe Glu Asn Val His Val Val Lys
145                     150                     155                     160
Asp Leu Glu Lys Met Glu Ile Tyr Gln Ser Gln Lys Gly
                      165                     170

```

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

```

Met Ile Gln Pro Ala Ser Leu Glu Glu Leu Ala Ser Leu Val Glu Lys
 1                      5                      10                      15
Ala Gly Lys Lys Val Phe Leu Phe Val Ala Asp Trp Cys Gly Asp Cys
                      20                      25                      30
Arg Tyr Ile Tyr Pro Ala Leu Pro Glu Ile Glu Glu Thr Asn Pro Glu
35                      40                      45
Phe Thr Phe Ile Arg Met Asp Arg Asp Gln Tyr Met Asp Leu Ala Lys
50                      55                      60
Leu Trp Asp Val Tyr Gly Ile Pro Ser Leu Val Val Leu Glu Lys Asp
65                      70                      75                      80
Lys Glu Ile Gly Arg Phe Val Asn Arg Asp Arg Lys Ser Lys Glu Gln
                      85                      90                      95
Ile Asn Asp Phe Leu Ala Gly Leu Lys
                      100                     105

```

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

```

Met Arg Leu Gly Leu Leu Gln Val Leu Arg Leu Pro Lys Ala Phe Gln
 1             5             10             15
Leu Ile Phe Ile Gln Asp Lys Gly His Gly Asp Val Ser Ser Phe Thr
             20             25             30
Ala Ser Cys Val Thr Gly Pro Trp Ala Phe Lys Leu Val Gly Lys Gln
             35             40             45
Gly Asn Ile His
             50

```

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```

Met Lys Thr Arg Lys Ile Pro Leu Arg Lys Ser Val Val Ser Asn Glu
 1             5             10             15
Val Ile Asp Lys Arg Asp Leu Leu Arg Ile Val Lys Asn Lys Glu Gly
             20             25             30
Gln Val Phe Ile Asp Pro Thr Gly Lys Ala Asn Gly Arg Gly Ala Tyr
             35             40             45
Ile Lys Leu Asp Asn Ala Glu Ala Leu Glu Ala Lys Lys Lys Lys Val
             50             55             60
Phe Asn Arg Ser Phe Ser Met Glu Val Glu Glu Ser Phe Tyr Asp Glu
             65             70             75             80

```

Leu Ile Ala Tyr Val Asp His Lys Val Lys Arg Arg Glu Leu Gly Leu
 85 90 95
 Glu

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Val | Ala | Tyr | Phe | Lys | Val | His | His | Pro | Ile | Tyr | Tyr | Tyr | Cys |
| 1 | | | | | 5 | | | | | 10 | | | | 15 | |
| Ala | Tyr | Phe | Ser | Ile | Arg | Ala | Lys | Ala | Phe | Asp | Ile | Lys | Thr | Met | Gly |
| | | | 20 | | | | 25 | | | | | | 30 | | |
| Ala | Gly | Leu | Glu | Val | Ile | Lys | Arg | Arg | Met | Glu | Glu | Ile | Ser | Glu | Lys |
| | | 35 | | | | | 40 | | | | | | 45 | | |
| Arg | Lys | Asn | Asn | Glu | Ala | Ser | Asn | Val | Glu | Ile | Asp | Leu | Tyr | Thr | Thr |
| | | 50 | | | | | 55 | | | | 60 | | | | |
| Leu | Glu | Ile | Val | Asn | Glu | Met | Trp | Glu | Arg | Gly | Phe | Lys | Phe | Gly | Lys |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Leu | Asp | Leu | Tyr | Cys | Ser | Gln | Thr | Thr | Glu | Phe | Leu | Ile | Asp | Gly | Asp |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Thr | Leu | Ile | Pro | Pro | Phe | Val | Ala | Met | Asp | Gly | Leu | Gly | Glu | Asn | Val |
| | | | 100 | | | | | | 105 | | | | | 110 | |
| Ala | Lys | Gln | Leu | Val | Arg | Ala | Arg | Glu | Glu | Gly | Glu | Phe | Leu | Ser | Lys |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Thr | Glu | Leu | Arg | Lys | Arg | Gly | Gly | Leu | Ser | Ser | Thr | Leu | Val | Glu | Lys |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Met | Asp | Glu | Met | Gly | Ile | Leu | Gly | Asn | Met | Pro | Glu | Ile | Thr | Ser | |
| 145 | | | | | | 150 | | | | | 155 | | | | |

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```

Met Ser Ser Lys Ile Ser Ile Gly Gln Leu Ile Thr Phe Asn Thr Leu
 1             5             10             15
Leu Ser Tyr Phe Thr Thr Pro Met Glu Asn Ile Ile Asn Leu Gln Thr
      20             25             30
Lys Leu Gln Ser Ala Lys Val Ala Asn Asn Arg Leu Asn Glu Val Tyr
 35             40             45
Leu Val Glu Ser Glu Phe Gln Val Gln Glu Asn Pro Val His Ser His
 50             55             60
Phe Leu Met Gly Asp Ile Glu Phe Asp Asp Leu Ser Tyr Lys Tyr Gly
65             70             75             80
Phe Gly Arg Asp Thr Leu Thr Asp Ile Asn Leu Thr Ile Lys Gln Gly
      85             90             95
Asp Lys Val Ser Leu Val Gly Val Ser Gly Ser Gly Lys Thr Thr Leu
      100             105             110
Ala Lys Met Ile Val Asn Phe Phe Glu Pro Tyr Lys Gly His Ile Ser
      115             120             125
Ile Asn His Gln Asp Ile Lys Asn Ile Asp Lys Lys Ser Leu Ala Pro
      130             135             140
Ser Tyr
145

```

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

```

Met Arg Gln Ala Pro Ala Leu Ala Gln Ala Asn Ile Glu Arg Val Val
 1             5             10             15
Val His Lys Ile Ser Lys Val Trp Glu Phe His Phe Arg Ile Phe
      20             25             30

```

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Lys Trp Tyr Tyr Leu Arg
 1             5             10             15
Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Glu Gly Thr Thr Trp
          20             25             30
Tyr Tyr Leu Asp Gln Pro Asn Gly Asp Met Lys Thr Gly Trp Gln Asn
      35             40             45
Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr
      50             55             60
Gly Trp Tyr Gln Glu Gly Thr Thr Trp Tyr Tyr Leu Asp Gln Pro Asn
65             70             75             80
Gly Asp Met Lys Thr Gly Trp Gln Asn Leu Gly Asn Lys Trp Tyr Tyr
          85             90             95
Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp Gly Ser
          100             105             110
Thr Trp Tyr Tyr Leu Asn Ala Val Met Glu Ile
      115             120

```

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```

Met Lys Trp Gly Ser Arg Ile Leu Leu Gly Leu Thr Pro Lys Ser Leu
 1             5             10             15

```

```

Arg Tyr Arg Ile Trp Lys Lys Ala Glu Lys Glu Met Thr Lys Tyr Asp
      20                      25                      30
Leu Ala Asp Cys Asp Gly Ile Thr Glu Leu Cys Ser Gly Pro Gly Tyr
      35                      40                      45
Met Arg Asn Lys Tyr Pro Ile Thr Ser Phe Glu Asp Asn Leu Phe Leu
      50                      55                      60
Pro Phe Glu Gly Thr Glu Met Pro Ile Pro Ile Gly Tyr Asp Val Tyr
      65                      70                      75                      80
Leu Arg Thr Ala Phe Gly Asp Tyr Met Thr Pro Pro Pro Ala Asp Lys
      85                      90                      95
Gln Val Pro His Gln Asp Ala Val Ile Ala Asp Met Asp Lys Ser Tyr
      100                     105                     110
Thr Glu Tyr Lys Gly Glu Tyr Gly Gly
      115                     120

```

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

```

Met Phe Pro Asp Ser Ile Asp Thr Met His Gln Ala Asn Glu Phe Ile
  1                      5                      10                      15
Ala Leu Asp Asp Leu Phe Arg Ala Ala Ile Tyr Ala Glu Ala Ile
      20                      25                      30
Tyr Glu Leu Ile Lys
      35

```

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

```

Met Asp Glu Leu Gln Lys Arg Asn Leu Leu Gly Phe Val Phe Gln Asp
 1             5             10             15
Phe Gln Leu Phe Pro His Leu Ser Val Leu Glu Asn Leu Thr Leu Ser
          20             25             30
Pro Val Lys Thr Met Gly Met Lys Gln Glu Glu Ala Glu Lys Lys Ala
          35             40             45
Ser Gly Leu Leu Glu Gln Leu Gly Leu Gly Gly His Ala Glu Ser Tyr
          50             55             60
Pro Phe Ser Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Leu Ala Arg
          65             70             75             80
Ala Met Met Ile Asp Pro Glu Ile Ile Gly Tyr Asp Glu Pro Thr Ser
          85             90             95
Ala Leu Asp Pro Glu Leu Arg Leu Glu Val Glu Lys Leu Ile Leu Gln
          100            105            110
Asn Arg Glu Leu Gly Met Thr His Ile Val Val Thr His Asp Leu Gln
          115            120            125
Phe Gly
          130

```

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

```

Met Tyr Gly Ala Asn Ser Glu Arg Leu Lys Glu Ser Leu Arg Ile Ser
 1             5             10             15
Leu Ser Pro Gln Asn Thr Val Glu Asp Leu Gln Thr Leu Ala Lys Thr
          20             25             30
Leu Lys Glu Ile Ile Gly Gly
          35

```

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```

Met Ile Ala Arg Ser Tyr Gln Glu Met Asp Asp Leu Asp Thr Ala Tyr
 1             5             10             15
Glu His Tyr Gln Glu Leu Thr Gly Asp Leu Lys Asp Asn Pro Glu Phe
          20             25             30
Leu Glu His Tyr Ile Tyr Leu Leu Arg
          35             40

```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```

Met Lys His Phe Asp Thr Ile Val Ile Gly Gly Gly Pro Ala Gly Met
 1             5             10             15
Met Ala Thr Ile Ser Ser Ser Phe Tyr Gly Gln Lys Thr Leu Leu Ile
          20             25             30
Glu Lys Asn Arg Lys Leu Gly Lys Lys Leu Ala Gly Thr Gly Gly Gly
          35             40             45
Arg Cys Asn Val Thr Asn Asn Gly Ser Leu Asp Asn Leu Leu Ala Gly
          50             55             60
Ile Pro Gly Asn Gly Arg Phe Leu Tyr Ser Val Phe Ser Gln Phe Asp
          65             70             75             80
Asn His Asp Ile Ile Asn Phe Phe Thr Glu Asn Gly Val Lys Leu Lys
          85             90             95
Val Glu Asp His Gly Arg Val Phe Pro Ala Ser Asp Lys Ser Arg Thr
          100            105            110
Ile Ile Glu Ala Leu Glu Lys Lys Ile Thr Glu Leu Gly Gly Gln Val
          115            120            125

```

Ala Thr Pro Asn Arg Asn Arg Phe Cys
130 135

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Leu | Ala | Lys | Asp | Ile | Ala | Ser | His | Leu | Leu | Lys | Ile | Gln | Ala |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Val | Tyr | Leu | Lys | Pro | Glu | Glu | Pro | Phe | Thr | Trp | Ala | Ser | Gly | Ile | Lys |
| | | | 20 | | | | 25 | | | | | 30 | | | |
| Ser | Pro | Ile | Tyr | Thr | Asp | Asn | Arg | Val | Thr | Leu | Ala | Tyr | Pro | Glu | Thr |
| | | 35 | | | | 40 | | | | | 45 | | | | |
| Arg | Thr | Leu | Ile | Glu | Asn | Gly | Phe | Val | Glu | Ala | Ile | Lys | Glu | Ala | Phe |
| | 50 | | | | 55 | | | | 60 | | | | | | |
| Pro | Glu | Val | Glu | Val | Ile | Ala | Gly | Thr | Ala | Thr | Ala | Gly | Ile | Pro | His |
| 65 | | | | 70 | | | | 75 | | | | | 80 | | |
| Gly | Ala | Ile | Ile | Ala | Asp | Lys | Met | Asp | Leu | Pro | Phe | Ala | Tyr | Ile | Pro |
| | | | 85 | | | | | 90 | | | | | 95 | | |

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Lys | Val | Leu | Ala | Ala | Cys | Gly | Asn | Gly | Met | Gly | Ser | Ser | Met |
| 1 | | | | 5 | | | | 10 | | | | 15 | | | |
| Val | Ile | Lys | Met | Lys | Val | Glu | Asn | Ala | Leu | Arg | Lys | Leu | Asn | Gln | Thr |
| | | | 20 | | | | | 25 | | | | 30 | | | |

```

Asp Phe Thr Val Asn Ser Cys Ser Val Gly Glu Ala Lys Gly Leu Ala
   35              40              45
Val Gly Tyr Asp Ile Val Ile Ala Ser Leu His Leu Ile Gln Glu Leu
   50              55              60
Glu Gly Arg Thr Asn Gly Lys Leu Ile Gly Leu Asp Asn Leu Met Asp
   65              70              75              80
Asp Lys Glu Ile Thr Glu Lys Leu Ser Gln Ala Ile Gln
              85              90

```

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```

Met Ser Met Phe Leu Asp Thr Ala Lys Ile Lys Val Lys Ala Gly Asn
  1              5              10              15
Gly Gly Asp Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Asn
              20              25              30
Gly Gly Pro Trp Gly Gly Asp Gly Gly Arg Gly Gly Asn Val Val Phe
              35              40              45
Val Val Asp Glu Gly Leu Arg Thr Leu Met Asp Phe Arg Tyr Asn Arg
              50              55              60
His Phe Lys Ala Asp Ser Gly Glu Lys Gly Met Thr Lys Gly Met His
   65              70              75              80
Gly Arg Gly Ala Glu Asp Leu Arg Val Arg Val Pro Gln Gly Thr Thr
              85              90              95
Val Arg Asp Ala Glu Thr Gly Lys Val Leu Thr Asp Leu Ile Glu His
              100              105              110
Gly Gln Glu Phe Ile Val Ala His Gly Gly Pro Trp Trp Thr Trp Lys
              115              120              125
Tyr Ser Phe Arg Asp Thr Lys Lys Ser Cys Thr Gly Asn Leu
              130              135              140

```

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

```

Met Met Lys Gly Glu Met Thr Phe Lys Gln Val His Tyr Lys Tyr Gly
 1           5           10           15
Tyr Gly Arg Asp Val Leu Ser Asp Ile Asn Leu Thr Val Pro Gln Gly
      20           25           30
Ser Lys Val Ala Phe Val Gly Ile Ser Gly Ser Gly Lys Thr Thr Leu
      35           40           45
Ala Lys Met Met Val Asn Phe Tyr Asp Pro Ser Gln Gly Glu Ile Ser
      50           55           60
Leu Gly Gly Val Asn Leu Asn Gln Ile Asp Lys Lys Ala Leu Arg Gln
65           70           75           80
Tyr Ile Ile Tyr Leu Pro Pro Gln Pro Tyr Val Phe Asn Gly Thr Ile
      85           90           95
Leu Glu Asn Leu Leu Leu Gly Ala Lys Gly Gly Asp Asp Thr Gly Lys
      100          105          110
Ile Ser Leu Thr Gly Arg Ser Glu Phe Gly Ser Glu Ile Pro Lys Arg
      115          120          125
Asn Ile Ser Lys Pro Pro Cys His Leu Glu Ile Tyr Gln Thr Glu Leu
      130          135          140
Thr Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Arg Gln Arg Ile Ala
145          150          155          160
Leu Ala Arg Ala Leu Leu Thr Asp Ala Pro Val Leu Ile Leu Asp Glu
      165          170          175
Ala Thr Asn Ser Leu Asp Ile Leu Thr Lys Lys Arg Ile Val His Tyr
      180          185          190
Leu Met Ala Leu Asp Lys Thr Phe Asp Phe His Cys Ser Pro Leu Asp
      195          200          205
Tyr Cys
      210
  
```

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

```

Met Ala Arg Phe Ile Glu Ile Asp Ala Lys Glu His Asp Arg Val Thr
 1             5             10             15
Ser Gln Ile Ser His Phe Pro His Ile Leu Ala Ser Ser Leu Met Glu
          20             25             30
Gln Thr Ala Val Tyr Ala Gln Glu His Glu Asn Gly Lys Ala Leu Cys
          35             40             45
Gly Arg Trp Phe Ser Arg Tyr Asp Pro Asn Cys Gly Lys Arg Ala Arg
          50             55             60
Asn Val Asp Leu His Ser Leu Val Gln
65             70

```

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

```

Met Ala His Gln Gly Gln Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile
 1             5             10             15
Lys Glu Asp Asn Leu Glu Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe
          20             25             30
Ile Asn Leu His His Asn Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr
          35             40             45
Glu Asp Leu Cys Ala Ser Phe Gln Ala Ala Val Leu Asp Ile Leu Met
          50             55             60
Ala Lys Thr Lys Lys Ala Leu Glu Lys Tyr Pro Val Lys Thr Leu Val
65             70             75             80
Val Ala Gly Gly Val Ala Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala
          85             90             95
Ala Glu Val Thr Asp Val Lys Val Ile Ile Pro Pro Leu Arg Leu Cys
          100            105            110
Gly Asp Asn Ala Gly Met Ile Ala Tyr Ala Ser Val Ser Glu Trp Asn
          115            120            125

```

Lys Glu Asn Phe Ala Asn Leu Asp Leu Asn Ala Lys Pro Ser Leu Ala
 130 135 140
 Phe Asp Thr Met Glu
 145

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Met Lys Arg Ser Leu Asp Ser Arg Val Asp Tyr Ser Leu Leu Leu Pro
 1 5 10 15
 Val Phe Phe Leu Val Ile Gly Val Val Ala Ile Tyr Ile Ala Val
 20 25 30
 Ser His Asp Tyr Pro Asn Asn Ile Leu Pro Ile Leu Gly Gln Gln Val
 35 40 45
 Ala Trp Ile Ala Leu Gly Leu Val Ile Gly Phe Val Val Met Leu Phe
 50 55 60
 Asn Thr Glu Phe Leu Trp Lys Val Thr Pro Phe Leu Tyr Ile Phe Arg
 65 70 75 80
 Leu Gly Thr Tyr Asp Leu Ala Asp Cys Ile Leu
 85 90

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Met Pro Asp Asp Ile Ile Asp Ser Phe Trp Tyr Ile Ile Asp His Phe
 1 5 10 15

```

Leu Lys Asn Val Phe Glu Leu Glu Glu Leu Glu Phe Gln Leu Leu
      20              25              30
Asn Asn Gln Gly Lys Ile Thr Phe His Phe Ser Ser Gln His Leu Pro
      35              40              45
Thr Ala Ile Asp Phe Asp Phe Asn His Pro Phe Asp Pro Arg Tyr Pro
      50              55              60
Pro Arg Val Leu Val Leu Asp Met Asp Gly Arg Glu Thr Ile Leu Leu
      65              70              75              80
Pro Glu Glu Asn Asp Leu Phe
              85

```

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

```

Met Gly Lys Lys Asp Ala Ser Ala Met His Glu Met Arg Ala Ser Phe
 1              5              10              15
Ile Gln Gly Ser Ile Glu Ala Gly His Thr Ala Glu Lys Ser Glu Gln
      20              25              30
Val Phe Asp Val Met Glu Lys Phe Ala Gly Tyr Gly Phe Asn Arg Ser
      35              40              45
His Ala Tyr Ala Tyr Ser Ala Leu Ala Phe Gln Leu Ala Tyr Phe Lys
      50              55              60
Thr His Tyr Pro Ala Ile Phe Tyr Gln Val Met Leu Asn Tyr Ser Asn
      65              70              75              80
Ser Asp Tyr Leu Ile Asp Ala Leu Glu Ala Gly Phe Glu Val Ala Ser
      85              90              95
Leu Ser Ile Asn Thr Ile Pro Tyr His Asp Lys Ile Ala Asn Lys Ser
      100             105             110
Ile Tyr Ile Gly Leu Lys Ser Ile Lys Gly Leu Gln Gln Gly Leu Gly
      115             120             125
Ala Leu Asp Tyr
      130

```

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

```

Met Asp Lys Lys Gln Asn Leu Thr Ser Phe Gln Glu Leu Thr Thr Thr
 1           5           10           15
Glu Leu Asn Gln Ile Thr Gly Gly Glu Trp Trp Glu Glu Leu Leu His
          20           25           30
Glu Thr Ile Leu Ser Lys Phe Lys Ile Thr Lys Ala Leu Glu Leu Pro
          35           40           45
Ile Gln Leu
          50

```

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

```

Met His Glu Met Phe Thr Ala Ile Ala Glu Ser Asp Met Lys Lys Ala
 1           5           10           15
Ala Ala Ile Gln Arg Lys Phe Ile Pro Lys Val Asn Ala Leu Phe Ser
          20           25           30
Tyr Pro Ser Pro Ala Pro Val Lys Ala Ile Leu Asn Tyr Met Gly Phe
          35           40           45
Glu Ala Gly Pro Thr Arg Leu Pro Leu Val Pro Ala Pro Glu Glu Asp
          50           55           60
Val Lys Arg Ile Ile Lys Val Val Val Asp Gly Asp Tyr Glu Ala Thr
          65           70           75           80
Lys Ala Thr Val Thr Gly Val Leu Arg Pro Asp Tyr
          85           90

```

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

```

Met Leu Asn Glu Phe Pro Ile Phe Asp Tyr Glu Asp Ile Gln Leu Ile
 1             5             10             15
Pro Asn Lys Cys Val Ile Lys Ser Arg Ala Glu Ala Asp Thr Ser Val
          20             25             30
Thr Leu Gly Asn His Thr Phe Lys Leu Pro Val Val Pro Ala Asn Met
          35             40             45
Gln Thr Ile Leu Asp Glu Asn Val Ala Glu Gln Leu Ala Lys Gly Gly
          50             55             60
Tyr Leu Tyr Thr Tyr Ala Pro Phe
65             70

```

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

```

Met Asp Ile Lys Leu Lys Asp Phe Glu Gly Pro Leu Asp Leu Leu Leu
 1             5             10             15
His Leu Val Ser Lys Tyr Gln Met Asp Ile Tyr Asp Val Pro Ile Thr
          20             25             30
Glu Val Ile Glu Gln Tyr Leu Ala Tyr Val Ser Thr Leu Gln Ala Met
          35             40             45
Arg Leu Glu Val Thr Gly Glu Tyr Met Val Met Ala Ser Gln Leu Met
          50             55             60

```

Leu Ile Lys Ser Arg Lys Leu Leu Pro Lys Val Ala Glu Val Thr Asp
 65 70 75 80
 Leu Gly Asp Asp Leu Glu Gln Asp Leu Leu Ser Gln Ile Glu Glu Tyr
 85 90 95
 Arg Lys Phe Lys Leu Leu Gly Glu His Leu Glu Ala Lys His Gln Glu
 100 105 110
 Thr Gly Pro Val Leu Phe Gln Ser Ala Asp Arg Val Asp Leu Arg Arg
 115 120 125
 Cys Gly Ala Cys Ala
 130

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Met Gln Ser Thr Glu Lys Lys Pro Leu Thr Ala Phe Thr Xaa Ile Ser
 1 5 10 15
 Thr Ile Ile Leu Leu Leu Leu Thr Val Leu Xaa Ile Phe Pro Phe Tyr
 20 25 30
 Trp Ile Leu Thr Gly Ala Phe Lys Ser Gln Pro Asp Thr Ile Val Ile
 35 40 45
 Pro Pro Gln Trp Phe Pro Lys Met Pro Thr Met Glu Asn Phe Gln Gln
 50 55 60
 Leu Met Val Gln Asn Pro Ala Leu Gln Trp Met Trp Asn Ser Val Phe
 65 70 75 80
 Ile Ser Leu Val Thr Met Phe Leu Val Cys Ala Thr Ser Ser Leu Ala
 85 90 95
 Gly Tyr Val Leu Ala Xaa Lys Arg Phe Tyr Gly Xaa Arg Ile Tyr Cys
 100 105 110

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

```

Met Leu Phe Met Arg Asp Ser Leu Asp Ser Ile Val Glu Pro Val Leu
 1             5             10             15
Asp Glu Met Gly Arg Phe Tyr Asp Trp Thr Glu Glu Glu Lys Ala Thr
      20             25             30
Tyr Arg Ala Asp Val Lys Ala Ala Leu Ala Gln Asn Asp Leu Ala Glu
      35             40             45
Leu Lys Asn
      50

```

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```

Met Lys Ile Lys Val Val Thr Val Gly Lys Leu Lys Glu Lys Tyr Leu
 1             5             10             15
Lys Asp Gly Ile Ala Glu Tyr Ser Lys Arg Ile Ser Arg Phe Ala Lys
      20             25             30
Phe Glu Met Ile Glu Leu Ser Asp Glu Lys Thr Pro Asp Lys Ala Ser
      35             40             45
Glu Ser Glu Asn Gln Lys Ile Leu Glu Ile Glu Gly Gln Arg Ile Leu
      50             55             60
Ser Lys Ile Ala Asp Arg Asp Phe Val Ile Val Leu Ala Ile Glu Gly
      65             70             75             80
Lys Thr Phe Phe Ser Glu Glu Phe Ser Lys Gln Leu Glu Glu Thr Ser
      85             90             95
Ile Lys Gly Xaa Ser Thr Leu Thr Phe Ile Ile Gly Gly Ser Leu Gly
      100            105            110
Leu Ser Ser Ser Val Lys Asn Arg Ala Asn Leu Ser Val Ser Phe Gly
      115            120            125

```

Arg Leu Thr Leu Pro His Gln Leu Met Arg Leu Val Leu Val Glu Gln
 130 135 140
 Ile Tyr Arg Ala Phe Thr Ile Gln Gln Gly Phe Pro Tyr His Lys
 145 150 155

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Met Gly Ile Leu Ala Trp Cys Asp Leu Val Leu Tyr Arg Leu Trp Asp
 1 5 10 15
 Ser Phe Met Asp Leu Gly Leu Phe Ile Asn Asp Ala Trp Val Arg Lys
 20 25 30
 Lys Lys Thr Leu Asn Lys Glu Arg Lys Lys Ala Gly Lys Ala Ala Leu
 35 40 45
 Pro Glu Asn Arg Trp Ile Gln Leu Leu Gly Met Val Val Thr Phe His
 50 55 60
 Val Val Met Leu Ser Phe Leu Ile Phe Ser Gly Phe Leu Asn Asn Leu
 65 70 75 80
 Trp Phe Lys Lys

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Met Val Met Ala Glu Asp Gln Ala Val Arg Gln Asn Arg Leu Ala Ile
 1 5 10 15

Leu Ser Gln Leu Thr Lys Lys Ala Ala Lys Phe Ala Cys Phe Asn Gln
 20 25 30
 Ile Asn Thr Lys
 35

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Met Gly Ala Gln Pro Val Gln Asp Thr Glu Thr Ser Ser Ala Leu Ile
 1 5 10 15
 Ser Ser His Tyr Leu Asp Glu Gln Asp Leu Ser Glu Lys Leu Lys Ser
 20 25 30
 Glu Leu Gln Trp Phe Glu Leu Glu Asn Lys Leu Leu Asn Leu Trp Glu
 35 40 45
 His

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Met Asp Glu Val Thr Ile Phe Gly Ile Asn Tyr Phe Lys Glu His Tyr
 1 5 10 15
 Pro Glu Lys Leu Ala Glu Arg Phe Lys Gln Met Lys Ile Glu Glu Glu
 20 25 30
 Ala Pro Val Ile Ile Met Asp Met Thr Arg Ala Leu Gly Phe Arg Asp
 35 40 45

Asp Tyr Asp Arg Phe Tyr Ser Leu Phe Arg Glu Gly Ser Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Met Lys Val Ile Asn Gln Thr Leu Leu Glu Lys Val Ile Ile Glu Arg
 1 5 10 15
 Ser Arg Ser Ser His Lys Gly Asp Tyr Gly Xaa Leu Leu Leu Leu Gly
 20 25 30
 Gly Thr Tyr Pro Tyr Gly Val Xaa Ser Ser Trp Leu Leu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Met Asn Trp Ile Leu Leu Gln Gly Leu Ile Cys Gln Arg Asp Ala Ser
 1 5 10 15
 Tyr Asp Met Lys Gln Asp Asp Leu Asp Lys Val Ala Asp Tyr Leu Phe
 20 25 30
 Lys Thr Glu Glu Trp Thr Met Tyr Glu Leu Ile Leu Phe Gly Asn Leu
 35 40 45
 Tyr Ser Phe Tyr Asp Val Asp Tyr Val Thr Arg Ile Gly Arg Glu Val
 50 55 60
 Met Glu Arg Glu Glu Phe Tyr Gln Glu Ile Ser Arg His Lys Arg Leu
 65 70 75 80

Val Leu Ile Leu Ala Leu Asn Cys Tyr Gln His Cys Leu Glu His Ser
 85 90 95
 Ser Phe Tyr Asn Ala Asn Tyr Phe Glu Ala Tyr Thr Glu Lys Ile Ile
 100 105 110
 Asp Lys Gly Ile Lys Leu Tyr Glu Arg Asn Val Phe His Tyr Leu Lys
 115 120 125
 Gly Phe Ala Leu Tyr Gln Lys Gly Gln Cys Lys Glu Gly Cys Lys Gln
 130 135 140
 Met Gln Glu Thr Met His Ile Phe Asp Val Leu Gly Leu Pro Glu Gln
 145 150 155 160
 Val Ser Leu Leu Ser Gly Thr Leu Arg Lys Ile Cys Gln Lys Leu Ile
 165 170 175
 Phe Pro Asn Lys Gly Lys Asn Lys Lys Leu Leu Ser Val Leu Ile Gln
 180 185 190

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Met Ser Thr Val Leu Ser Trp Thr Ala Tyr Lys Thr Gln Arg Leu Glu
 1 5 10 15
 Met Ser Ile Leu Leu His Met Ile Val Asn Gly Ile Ala Phe Cys Leu
 20 25 30
 Leu Ala Leu Val Val Ile Met Ser Arg Thr Leu Gly Ile Ser Val
 35 40 45

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

```

Met Arg Glu Asn Asp Leu Leu Leu Ile Thr Ala Asp His Gly Asn Asp
 1             5             10             15
Pro Thr Tyr Ala Gly Thr Asp His Thr Arg Glu Tyr Ile Pro Leu Leu
      20             25             30
Ala Tyr Ser Pro Ala Phe Lys Gly Asn Gly Leu Ile Pro Val Gly His
      35             40             45
Phe Ala Asp Ile Ser Ala Thr Val Ala Asp Asn Phe Gly Val Glu Thr
      50             55             60
Ala Met Ile Gly Glu Ser Phe Leu Asp Lys Leu Val
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

```

Met Lys Lys Ile Phe Leu Thr Leu Leu Thr Val Ser Leu Leu Gly Gly
 1             5             10             15
Ala Ser Thr Ala Val Ala Gln Asp Phe Thr Ile Ala Ala Lys His Ala
      20             25             30
Ile Ala Val Glu Ala Asn Thr Gly Lys Ile Leu Tyr Glu Lys Asp Ala
      35             40             45
Thr Pro Pro Val Glu Ile Ala Ser Ile Thr Lys Leu Ile Thr Val Tyr
      50             55             60
Leu Val Tyr Glu Ala Leu Glu Asn Gly Ser Ile Thr Leu Ser Thr Pro
65             70             75             80
Val Asp Ile Ser Asp Tyr Pro Tyr Gln Leu Thr Thr Asn Ser Glu Ala
      85             90             95
Ser Asn Ile Pro Met Glu Ala Arg Asn Tyr Thr Val Glu Glu Leu Leu
      100            105            110
Glu Ala Thr Leu Val Ser Ser Ala Asn Ser Ala Ala Ile Ala Leu Ala
      115            120            125
Glu Lys Ile Ala Gly Ser Glu Lys Asp Phe Val Xaa Met Met Arg Ala
      130            135            140

```

Lys Leu Leu Glu Trp Gly Ile Arg Ile His Cys Cys Gln Tyr Asp Arg
 145 150 155 160
 Ser

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

Met Ser Asn Ala Met Glu Gly Val Leu Tyr Phe Leu Lys Pro Asp Phe
 1 5 10 15
 Ser Lys Leu Thr Ser Ala Asp Leu Leu Tyr Ala Leu Gly Gln Ser Phe
 20 25 30
 Phe Ala Leu Ser Leu Gly Val Thr Asp Met Leu Thr Tyr Ala Ser Tyr
 35 40 45
 Leu Asp Lys Lys Thr Asn Leu Val Gln Ser Gly Ile Ser Ile Val Thr
 50 55 60
 Met Asn Ile Ser Ile Val His His Gly Arg Ser Ser His Phe Pro Ser
 65 70 75 80
 His Val Ser Leu Gln Tyr Pro Leu
 85

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Met Lys Val Ala Lys Pro Phe Trp Ala Ile Val Lys Leu Lys Ser Val
 1 5 10 15

Gln His Ala Ser Met Leu Glu Asn Pro Lys Glu Met Asp Gly Leu Met
 20 25 30
 Lys Gln Val Glu Asn Leu Ala Leu Glu Asn Gln Gly Tyr Gln Val Glu
 35 40 45
 Lys Glu Asn Lys Ala Phe Glu Gln Ile Lys Asp Ser Val Ala Thr Phe
 50 55 60
 Gln Thr Phe Leu Thr Ile Phe Leu Tyr Gly Cys
 65 70 75

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Met Asp Ala Glu Val Ser Lys Asn Leu Arg Leu Ile Leu Glu Arg Lys
 1 5 10 15
 Gly Met Thr Ile Leu Thr Gly Thr Lys Leu Gln Glu Ile Ile Glu Glu
 20 25 30
 Asn Gly Gln Leu Arg Ile Lys Val Glu Gly Lys Asp Asn Ile Ile Ala
 35 40 45
 Ser Lys Ala Leu Leu Ser Ile Gly Arg Met Pro Asp Leu Glu Gly Ile
 50 55 60
 Gly Glu Val Glu Phe Glu Leu Asp Arg Gly Cys Ile Lys Val Asn Glu
 65 70 75 80
 Tyr Met Glu Thr Ser Val Pro Arg Ile Tyr Ala Thr Arg
 85 90

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

```

Met Lys Asn Ser Ile Met Asp Thr Lys Phe Asp Arg Arg Ile Leu Leu
 1             5             10             15
Leu Asn Lys Ile Ile Ile Val Phe Ile Val Leu Met Thr Leu Leu Pro
          20             25             30
Leu Leu Tyr Ile Val Val Ala Ser Phe Met Asp Pro Lys Val Leu Val
          35             40             45
Ser Arg Gly Ile Ser Phe Asn Pro Ala Asp Trp Thr Val Glu Gly Tyr
          50             55             60
Gln Arg Val Ile Gln
65

```

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

```

Met Val Ile Pro Glu Ala Gly Tyr Leu Tyr Ala Phe His Tyr Pro Asn
 1             5             10             15
Leu Lys Gly Lys Gly Lys Glu Ala Val Gln Val Ile Tyr Asn Leu Asn
          20             25             30
Leu Ala Ser Ala Lys Val Ile Gln Leu Tyr Arg Ser Leu Gly Leu Asp
          35             40             45
Gly Lys Ile Gly Ile Ile Leu Asn Leu Thr Pro Ala Tyr Pro Arg Ser
          50             55             60
Asn Ser Pro Glu Asp Leu Glu Ala Ser Arg Phe Thr Asp Asp Phe Phe
65             70             75             80
Asn Lys Val Phe Leu Glu Ser Ser Cys
          85

```

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

```

Met Thr Arg Ile Ala Ser Val Ser Val Ile Arg Asn Ala Ala Phe Ile
 1           5           10           15
Ala Ile Ala Leu Ser Phe Leu Gly Lys Phe Thr Ala Leu Ile Ser Thr
          20           25           30
Ile Pro Asn Ala Val Leu Gly Gly Met Ser Ile Leu Leu Tyr Gly Val
          35           40           45
Ile Ala Ser Asn Gly Leu Lys Val Leu Ile Lys Glu Arg Val Asp Phe
          50           55           60
Ala Gln Met Arg Asn Leu Ile Ile Ala Ser Ala Met Leu Val Leu Gly
65           70           75           80
Leu Gly Arg Ser Tyr Pro
          85

```

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```

Met Ser Leu Arg Glu Lys Ser Met Ser Glu Tyr Lys Leu Ser Glu Asn
 1           5           10           15
Asn Trp Thr Arg Val Ala Val Phe Ala Gly Gly Asn Arg Gly His Tyr
          20           25           30
Arg Thr Asp Phe Asp Ala Phe Val Gly Val Asp Arg Gly Ser Leu Trp
          35           40           45
Val Leu Glu Glu Asp Leu Pro Leu Ala Leu Ala Val Gly Asp Phe Asp
          50           55           60
Ser Val Thr Glu Glu Glu Arg Gln Val Ile Gln Lys Arg Ala Gln Tyr
65           70           75           80
Phe Val Gln Ala Arg Pro Glu Lys Asp Asp Thr Asp Leu Glu Leu Ala
          85           90           95

```

Leu Leu Thr Ile Phe Glu Gln Asn Pro Gln Ala Glu Val Thr Ile Phe
 100 105 110
 Gly Ala Leu Gly Gly Arg Ile Asp His Met Leu Ala Asn Val Leu Ser
 115 120 125
 Thr

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Met Val Leu Gln Arg Asn Glu Ile Asn Glu Lys Asp Thr Trp Asp Leu
 1 5 10 15
 Ser Thr Ile Tyr Pro Thr Asp Gln Ala Trp Glu Glu Ala Leu Lys Asp
 20 25 30
 Leu Thr Glu Gln Leu Glu Thr Val Ala Gln Tyr Glu Gly His Leu Leu
 35 40 45
 Asp Ser Ala Asp Asn Leu Leu Val Asn His
 50 55

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Met Ile Tyr Gly Ala Ile Ile Asp Ala Lys Thr Ala Glu Asn Ala Ala
 1 5 10 15
 Gly Met Thr Ala Met Gln Thr Ala Thr Asp Asn Ala Lys Lys Val Ile
 20 25 30
 301

Asn Asp Leu Thr Ile Gln Tyr Asn Arg Ala Gln Thr Gly Gly Tyr Tyr
 35 40 45
 Thr Arg Asn Tyr Arg Asn Arg Ser Ser Ala
 50 55

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met Thr Asp Gly Tyr Glu His Tyr Lys Lys Ile Met Glu Asn Pro Pro
 1 5 10 15
 Lys Asn Leu Ile Phe Pro Gly Ile Val Ser Pro Glu Arg Met Arg Glu
 20 25 30
 Ile Val Cys Ser Asn Gly Ser Phe Leu Val Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Met Ser Lys Gln Lys Lys Phe Glu Glu Asn Leu Ala Glu Leu Glu Thr
 1 5 10 15
 Ile Val Gln Ser Leu Glu Asn Gly Glu Ile Ala Leu Glu Asp Ala Ile
 20 25 30
 Thr Ala Phe Gln Lys Gly Met Val Leu Ser Lys Glu Leu Gln Ala Thr
 35 40 45
 Leu Asp Lys Ala Glu Lys Thr Leu Val Lys Val Met Gln Glu Asp Gly
 50 55 60

Thr Glu Ser Asp Phe Glu

65

70

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

```

Met Phe Ala Ala Val Thr Ala Gly Tyr Gln Ala Ala Leu Met Val Pro
 1             5             10             15
Thr Glu Ile Leu Ala Glu Gln His Phe Glu Ser Leu Gln Asn Leu Phe
      20             25             30
Pro Asn Leu Lys Leu Ala Leu Leu Thr Gly Ser Leu Lys Ala Ala Glu
      35             40             45
Lys Arg Glu Val Leu Glu Thr Ile Ala Lys Gly Glu Ala Asp Leu Ile
      50             55             60
Ile Gly Thr His Ala Leu Ile Gln Asp Gly Val Glu Tyr Ala Arg Leu
65             70             75             80
Gly Leu Ile Ile Ile Asp Glu Gln His Arg Phe Gly Val Gly Gln Arg
      85             90             95
Arg Ile Leu Arg Glu Lys Gly Asp Asn Pro Asp Val Leu Met Met Thr
      100            105            110
Ala Thr Pro Ile Pro Arg Thr Leu Ala Ile Thr Ala Phe Gly Asp Met
      115            120            125
Asp Val Ser Ile Ile Asp Gln Met Pro Ala Gly Arg Lys Pro Tyr Cys
      130            135            140
Asp Ala Leu Asp Gln Thr
145            150

```

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

```

Met Asn Arg Glu Ala Leu Arg Leu Tyr Leu Val Thr Asn Arg Tyr Gln
 1             5             10             15
Asp Ser Val Glu Ser Phe Leu Ala Lys Val Glu Thr Ala Cys Arg Ser
      20             25             30
Gly Val Thr Ile Val Gln Leu Arg Glu Lys Asn Leu Thr Thr Asn Gln
      35             40             45
Tyr Tyr Gln Leu Ala Lys Gln Val Lys Glu Ile Thr Asp Ala Tyr Gln
      50             55             60
Val Pro Leu Ile Ile Asp Asp Arg Leu Asp Val Cys Leu Ala Val Asp
      65             70             75             80
Ala Ala Gly Leu His Ile Gly Asp Asp Glu Leu Pro Val Ser Val Ala
      85             90             95
Arg Gln Val Leu Gly Pro Glu Lys Ile Pro Arg Cys His Arg
      100             105             110

```

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

```

Met Gln Gly Ser His Phe His Leu Pro Ile Tyr Arg Met Thr Ser Gln
 1             5             10             15
Ala Leu Leu Asp Glu Thr Lys Lys Val Ala Ile Pro Val Leu Ala Thr
      20             25             30
Thr Gln Ser Lys Asp Ser Val Asp Tyr Arg Glu Leu Pro Ser Ile Glu
      35             40             45
Asn Phe Val Leu Val Met Gly Asn Glu Gly Gln Gly Ile Ser Pro Leu
      50             55             60
Met Ala Glu Ser Ala Asp Gln Leu Val His Ile Ser Met Lys Gly Gln
      65             70             75             80
Ala Glu Ser Leu Asn Val Ala Val Ala Ala Gly Ile Leu Ile Phe His
      85             90             95
Leu Ser

```

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

```

Met Thr Lys Thr Ala Phe Leu Phe Ala Gly Gln Gly Ala Gln Tyr Leu
 1             5             10             15
Arg Met Gly Arg Asp Phe Tyr Asp Gln Tyr Pro Ile Val Lys Glu Thr
      20             25             30
Ile Asp Arg Ala Ser Gln Val Leu Gly Tyr Asp Leu Arg Tyr Leu Ile
      35             40             45
Asp Thr Glu Glu Asp Lys Leu Asn Gln Thr Arg Tyr Thr Gln Pro Ala
      50             55             60
Ile Leu Ala Thr Ser Val Ala Ile Tyr Arg Leu Leu Gln Glu Lys Gly
      65             70             75             80
Tyr His Pro Asp Met Val Ala Gly Leu Ser Leu Gly Glu Tyr Ser Ala
      85             90             95
Leu Val Ala Ser Gly Ala Leu Asp Phe Glu Asp Ala Val Ala Leu Val
      100            105            110
Ala Lys Arg Gly Ala Tyr Met Glu Glu Ala Ala Pro Ala Asp Ser Gly
      115            120            125
Lys Met Val Ala Val Leu His Thr Pro
      130            135

```

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Met Tyr Gln Phe Ser Gly Gln Thr Lys Val Xaa Glu Val Leu Ala Phe
 1 5 10 15
 Arg Asp Lys Pro Pro Tyr Gly Gly Ser Ser Ala Met Pro Leu Arg Cys
 20 25 30
 Leu

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Met Thr Lys Glu Thr Gly Met Glu Gln Thr Phe Phe Ile Ile Lys Pro
 1 5 10 15
 Asp Gly Val Lys Arg Gly Leu Val Gly Glu Val Leu Lys Arg Ile Glu
 20 25 30
 Gln Arg Gly Phe Thr Ile Glu Lys Leu Glu Phe Arg Ser Gln Val Phe
 35 40 45
 Arg Arg Val Asp
 50

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

Met Thr Ser Gly Pro Val Leu Val Gly Val Ile Ser Gly Pro Lys Val
 1 5 10 15

Ile Glu Thr Trp Arg Thr Met Met Gly Ala Thr Arg Pro Glu Glu Ala
 20 25 30
 Leu Pro Gly Thr Ile Arg Gly Asp Phe Ala Lys Ala Ala Gly Glu Asn
 35 40 45
 Glu Ile Ile Gln Asn Val Val His Gly Ser Asp Ser Glu Lys Asn Gln
 50 55 60
 Leu Ser Arg Glu Ile Ala Pro Leu Val Leu Arg Val Asp Trp Leu Asn
 65 70 75 80
 Gln Leu Asp Lys Ser Ser Phe Glu
 85

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

Met Gly Leu Lys Asp Asn Ala Gly Leu Val Lys Glu Tyr Ala Leu Val
 1 5 10 15
 Asp Ala Val Glu Tyr Gln Asn Val Ile Val Ala Thr Thr Val Glu Glu
 20 25 30
 Met Leu Ser Lys Tyr Ala Asn Lys Asn Asp Leu Glu Ile Asp Asn Ala
 35 40 45
 Thr Thr Glu Ser Ile Lys Gly Val Val Ala Asp Leu Lys Ser Ala Val
 50 55 60
 Ile Lys Gly Asp Thr Val Tyr Phe Phe Lys Val Asp Gly Lys Ile Tyr
 65 70 75 80
 Lys Val Lys Ala Ser Val Ser Asp Asp Leu Pro Tyr Leu Glu Asn Gly
 85 90 95
 Lys Thr Phe Glu Gly Gln Val Xaa Lys Asp Asn Tyr Leu Lys Thr Phe
 100 105 110
 Lys Val Gln
 115

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```

Met Ile Ser Gly Ser Glu Ile Arg Asp Ile Val Thr Ser Asp Ile Pro
 1             5             10             15
Leu Ala Asp Lys Thr Glu Thr Leu Val Arg Phe Ala Asn Asn Ala Gly
      20             25             30
Gly Leu Asp Asn Ile Thr Val Ala Leu Val Ser Met Asn Glu Glu Asp
      35             40             45
Glu Glu
      50

```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```

Met Pro Asp Asn Leu Ala Leu Arg Met Arg Pro Lys Thr Ile Asp Gln
 1             5             10             15
Val Ile Gly Gln Glu Xaa Leu Val Gly Pro Gly Lys Ile Ile Arg Arg
      20             25             30
Met Val Glu Ala Asn Arg Leu Ser Ser Met Ile Leu Tyr Gly Pro Pro
      35             40             45
Gly Ile Gly Lys Thr Ser Ile Ala Ser Ala Ile Ala Gly Thr Thr Lys
      50             55             60
Tyr Ala Phe Arg Thr Phe Asn Ala Thr Val Asp Ser
      65             70             75

```

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

```

Met Pro Glu Glu Leu Ala Tyr Leu Val Gln His Leu Asp Asn Ala Gln
 1             5             10             15
Glu Gln Val Val Leu Gly Asn Thr Tyr His Thr Gly Asn His Cys Phe
          20             25             30
Ser

```

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

```

Met Val Phe Trp Glu Gly Leu Val Pro Thr Pro Asp Val Ile Asp Ala
 1             5             10             15
Gly His Val Thr Gly Phe Leu Tyr Thr Val His Ser Ser Ser Thr Gly
          20             25             30
Leu Ile Val Leu Gln Ile Lys Lys Asp Leu Leu Lys Leu
          35             40             45

```

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

```

Met Thr Asp Arg Tyr Asp Ser Ser Leu Gly Ile Tyr Lys Val Pro Trp
 1           5           10           15
Cys Val Ser Gln Gln Gln Thr Val Thr Glu Ile Met Asp Thr Tyr Cys
          20           25           30
Asp Trp Gly Val Lys Tyr Pro Leu Val Tyr Leu Glu Asp Pro Phe Ser
        35           40           45
Asp Glu Asp Leu Asp Ser Trp Arg Lys Phe Gln Leu Ile Lys Pro Leu
        50           55           60
Lys Leu Gln Val Phe Gly Asp Asp Phe Tyr Ala Thr Asn Leu Glu Arg
        65           70           75           80
Ile Ser Gln Phe Lys Asp Cys Ala Asp Gly Ile Val Ile Lys Pro Asn
          85           90           95
Gln Val Gly Ser Val Ser Lys Thr Leu Glu Val Met Glu Tyr Ala Glu
          100          105          110
Lys Ser Gly Ile Ser Met Ala Phe Ser Gln Arg Thr Ala Glu Thr Glu
          115          120          125
Asn Asn Ile Ile Ser His Leu Ala Met Ser Val Ile Leu Leu Ile
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

```

Met Lys Lys Ile Ser Lys Gln Glu Leu Val Asn Thr Arg Phe Ser Arg
 1           5           10           15
Leu Phe Ala His Phe Gly Gln Glu Lys Asp Gly Ser Phe Leu Ala Gln
          20           25           30
Arg Tyr Gln Phe Tyr Leu Ala Gln Gln Gly Gln Thr Leu Ser Gly Ala
          35           40           45
His Asp Leu Leu Asp Ser Leu Ile Glu Arg Asp Tyr Asn Leu Tyr Ala
          50           55           60
Ala Thr Asn Gly Ile Thr Ala Ile Gln Thr Gly Arg Leu Ala Gln Ser
          65           70           75           80

```

Gly Leu Ala Pro Tyr Phe Asn Gln Val Phe Ile Ser Glu Gln Leu Gln
 85 90 95
 Thr Gln Lys Pro Asp Ala Leu Phe Tyr Glu Lys Ile Gly Gln Gln Ile
 100 105 110
 Ala Gly Phe Ser Lys Glu Lys Thr
 115 120

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Met His Arg Lys Thr Val Ile Asp Xaa Arg Thr Leu Gly Glu Arg Tyr
 1 5 10 15
 Thr Phe Thr Xaa Pro Ile Lys Glu Leu Lys Thr Arg Asn Val Ala Glu
 20 25 30
 Val Ala Asp Leu Leu Ala Xaa Val Glu Ser Tyr Gln Glu Gln Asp Tyr
 35 40 45
 Tyr Val Val Gly Tyr Val Ser Tyr Glu Ala Ala Pro Ala Phe Glu Glu
 50 55 60
 Lys Leu Ala Val His Lys Val Pro Leu Leu Gly Glu Tyr Leu Leu Tyr
 65 70 75 80
 Phe Thr Val His Asp Arg Val Glu Thr Ser Pro Ile Pro Leu Thr Tyr
 85 90 95
 Glu Asp Ile Asp Leu Pro Ser Asn Trp Gln Gly Xaa Asn Val Cys Thr
 100 105 110
 Glu Leu

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

```

Met Glu Arg Ile Glu Val Arg Ser Arg Ser Gly Ser Ala His Leu Gly
 1             5             10             15
His Val Phe Thr Asp Gly Pro Arg Glu Leu Gly Gly Leu Arg Tyr Cys
             20             25             30
Ile Asn Ser Ala Ser Leu Arg Phe Val Ala Lys Asp Glu Met Glu Lys
             35             40             45
Ala Gly Tyr Gly Tyr Leu Leu Pro Tyr Leu Asn Lys
             50             55             60

```

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

```

Met Glu Trp Ile Arg Leu Ile Gly Ile Ala Ile Ile Val Val Gly Phe
 1             5             10             15
Ile Leu Lys Phe Asp Thr Ile Ala Thr Val Val Leu Ala Gly Leu Val
             20             25             30
Thr Ala Leu Val Ser Gly Val Ser Leu Val Glu Phe Leu Glu Ile Leu
             35             40             45
Gly Lys Glu Phe Ser Asn Gln Arg Val Leu Thr Ile Phe Met Val Thr
             50             55             60
Leu Pro Leu Val Gly Leu Ser Glu Thr Phe Gly Leu Asn Asn Asp Gln
             65             70             75             80
Ser Ile

```

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

```

Met Leu Leu Ile Phe Ala Val Ile Gly Val Leu Val Ala Leu Ile Ala
 1             5             10             15
Gln Phe Tyr Ser Ala Lys Ala Ala Val Gly Phe Ala Lys Glu Leu Thr
      20             25             30
Asn Asp Leu Tyr Arg His Ile Leu Ser Leu Pro Lys Asp Ser Arg Asp
      35             40             45
Arg Leu Thr Thr Ser Ser Leu Val Thr Arg Leu Thr Ser Asp Thr Tyr
      50             55             60
Gln Ile Gln Thr Gly Ile Asn Gln Phe Leu Arg Leu Phe Leu Arg Ala
      65             70             75             80
Pro Ile Ile Val Phe Gly Ala Ile Phe Met Ala Tyr Arg Ile Ser Ala
      85             90             95
Glu Leu Thr Phe Trp Phe Leu Val Met Val Ala Ile Leu Thr Ile Val
      100            105            110
Ile Val Arg Val Ile Ser Ile Gly Gln Ser Ser Leu Gln
      115            120            125

```

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

```

Met Pro Ile Glu Gln Val Gln Lys Leu Leu Gly His Ser Lys Ile Asp
 1             5             10             15
Thr Thr Leu Ala Tyr Ala Met Val Asn Gln Asn Asn Val Lys His Ser
      20             25             30
His Gln Lys Phe Ile Ser
      35

```

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```

Met Lys Pro Cys Trp Lys Lys Cys Phe Pro Glu Glu Val Ser Ser Glu
 1             5             10             15
Gly Glu Val Thr Leu Ile Glu Ile Pro Val Ser Asp Lys Ile Ala Gly
          20             25             30
Lys Gln Val His Glu Leu Asn Leu Pro His Asn Val Leu Ile Thr Thr
          35             40             45
Gln Val His Asn Gly Lys Ser Gln Thr Val Asn Gly Ser Thr Arg Met
          50             55             60
Tyr Leu Gly Asp Met Ile His Leu Val Ile Pro Lys Ser Glu Ile Gly
65             70             75             80
Lys Val Lys Asp Leu Leu Leu
                      85

```

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

```

Met Asn Glu Gly Val Glu Asn Phe Arg Ala Lys Leu Ala Ser Leu Gly
 1             5             10             15
Ala Lys Asn Ile Gly Ile Tyr Val Gly Val Tyr Phe Met Glu Glu His
          20             25             30
Ser Ile Asp Thr Gly Lys Phe Thr Ser Val Trp Ile Pro Ser Tyr Gly
          35             40             45
Ser Asp Ser Gly Phe Leu Glu Ser Ser Pro Lys Thr Asp Leu Asp Tyr
50             55             60

```

Asp Ile His Gln Tyr Thr Ser Lys Gly Lys Leu Pro Ala Leu Thr Thr
 65 70 75 80
 Ile

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Met Val Ser Lys Tyr Leu Leu Leu Ala Val Ile Phe Ser Gly Leu Val
 1 5 10 15
 Thr Trp Ile Leu Arg Met Ile Ser Phe Ile Leu Val Lys Tyr Lys Gly
 20 25 30
 Leu Pro Ala Ile Val Glu Arg Phe Leu Lys Phe Leu Pro Val Ser Ile
 35 40 45
 Ile Phe Ala Leu Ile Leu Ser Ser Val Val Thr Gly Lys Val Gly Ser
 50 55 60
 Leu Pro Gln Ile Lys Trp Leu Asp Phe Leu Ala Val Phe Pro Thr Ala
 65 70 75 80
 Trp Val Ala Phe Arg Tyr Arg Asn Leu Leu Gly Thr Val Leu Phe Gly
 85 90 95
 Val Val Leu Ile Ala Ile Leu Arg Leu Val Ser
 100 105

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

```

Met Glu Asp Xaa Glu Thr Gln Arg Val Val Met Gln Tyr Arg Ala Pro
 1              5              10              15
Glu Asn Asn Arg Trp Ser Gly Tyr Ala Phe Pro Gly Gly His Val Glu
      20              25              30
Asn Asp Glu Ala Phe Ala Glu Ser Val Ile Arg Glu Ile Tyr Glu Glu
      35              40              45
Thr Gly Leu Thr Ile Gln Asn Pro Gln Leu Val Gly Ile Lys Asn Trp
      50              55              60
Pro Leu Asp Thr Gly Gly Arg Tyr Ile Val Ile Cys Tyr Lys Ala Thr
      65              70              75              80
Glu Phe Ser Gly Thr Leu Gln Ser Ser Glu Glu Gly Glu Val Ser Trp
      85              90              95
Val Gln Lys Asp Gln Ile Pro Asn Leu Asn Leu Ala Tyr Asp Met Leu
      100              105              110
Pro Leu Met Glu Met Met Glu Ala Pro Asp Lys Ser Glu Phe Phe Tyr
      115              120              125
Pro Arg Arg Thr Glu Asp Asp Trp Glu Lys Lys Ile Phe
      130              135              140

```

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

```

Met Thr Ile Glu Leu Leu Thr Pro Phe Thr Lys Val Glu Leu Glu Pro
 1              5              10              15
Glu Ile Lys Glu Lys Lys Arg Lys Gln Val Gly Ile Leu Gly Gly Asn
      20              25              30
Phe Asn Pro Val His Asn Ala His Leu Ile Val Ala Asp Gln Val Arg
      35              40              45
Gln Gln Leu Gly Leu Asp Gln Val Leu Leu Met Pro Glu Tyr Gln Pro
      50              55              60
Pro His Val
      65

```

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

```

Met Lys Lys Leu Val Phe Val Cys Leu Gly Asn Ile Cys Arg Ser Pro
 1             5             10             15
Met Ala Glu Phe Val Met Lys Ser Met Thr Asp Asn Tyr Glu Ile Gln
          20             25             30
Ser Arg Ala Thr Ser Ser Trp Glu His Gly Asn Pro Ile His Lys Gly
          35             40             45
Thr Gln Gly Ile Phe Gln Glu Tyr Glu Ile Pro Tyr Asp Lys Asn Lys
          50             55             60
Thr Ser Leu Gln Ile Ser Lys Glu Asp Phe Glu Ala Phe Asp Tyr Ile
          65             70             75             80
Ile Gly Met Asp Ala Ser Asn Val Pro Thr Tyr Val Arg Cys Val Gln
          85             90             95

```

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

```

Met Val Lys Tyr Gly Val Val Gly Ala Gly Tyr Phe Gly Ala Glu Leu
 1             5             10             15
Ala Arg Tyr Met Gln Lys Asn Asp Gly Ala Xaa Ile Thr Leu Leu Tyr
          20             25             30
Asp Pro Asp Asn Ala Glu Ala Ile Ala Glu Glu Leu Gly Ala Lys Val
          35             40             45
Ser Lys Phe Leu Arg
          50

```

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

```

Met Leu Trp Lys Tyr Tyr Asn Ser Ser Phe Leu Lys Ala Val Pro His
 1             5             10             15
Leu Thr Thr Glu Tyr Lys Arg Leu Ala Gln Ala His Gly Leu Asn Leu
          20             25             30
Lys Gln Ala Lys Pro Ile Thr Met Gly Met Trp Ile Gly Gly Asp Arg
          35             40             45
Glu Gly Asn Pro Phe Val Thr Ala Lys Asn Leu Lys Gln Ser Ala Leu
          50             55             60
Thr Gln Cys Glu Val Xaa Leu Asn Leu Leu
65             70

```

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

```

Met Asn Thr Leu Tyr Leu Asn Gln His Ser Ser Tyr Lys Asn Asp Glu
 1             5             10             15
Asp Ser His Ser Phe Pro Ile Gln Met Glu Leu Val Ser Asp Glu Met
          20             25             30
Ile Pro Arg Asn
          35

```

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

```

Met Ala Arg Lys Glu Thr Met Ala Glu Arg Lys Tyr Cys Lys Met Lys
 1             5             10             15
Lys Asp Ile His Pro Glu Tyr Arg Pro Val Val Phe Met Asp Thr Thr
             20             25             30
Thr Gly Tyr Gln Phe Leu Ser Gly Ser Thr Lys Arg Ser Asn Glu Thr
             35             40             45
Val Glu Phe Glu Gly Glu Thr Tyr Pro Leu Ile Arg Val Glu Ile Ser
             50             55             60
Ser Asp Ser His Pro Phe Tyr Thr Gly Arg Gln Lys Phe Thr Gln Ala
65             70             75             80
Asp Gly Arg Val Asp Arg Phe Asn Lys Lys Tyr Gly Leu Lys
             85             90

```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```

Met Glu Thr Ala Leu Ile Ser Val Ile Val Pro Val Tyr Asn Val Ala
 1             5             10             15
Gln Tyr Leu Glu Lys Ser Ile Ala Ser Ile Gln Lys Gln Thr Tyr Gln
             20             25             30
Asn Leu Glu Ile Ile Leu Val Asp Asp Gly Ala Thr Asp Glu Ser Gly
             35             40             45
Arg Leu Cys Asp Ser Ile Ala Glu Gln Asp Asp Arg Val Ser Val Leu
50             55             60

```

(2) INFORMATION FOR SEQ ID NO:434:

(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

(2) INFORMATION FOR SEQ ID NO:435:

(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

320

Lys Arg Val Asp Val Glu Ile Leu Glu Gly Leu Asp Asp Glu Asp
 50 55 60

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Met Asp Asp Asp Phe Lys Arg Tyr Asn Ala Pro Ile Leu Thr Trp Tyr
 1 5 10 15
 Glu Thr Ala Arg Tyr Ala Phe Glu Arg Gly Met Val Trp Gln Asn Leu
 20 25 30
 Gly Gly Val Glu Asn Ser Leu Asn Gly Gly Leu Tyr His Phe Lys Glu
 35 40 45
 Lys Phe Asn Pro Thr Ile Glu Glu Tyr Leu Gly Glu Phe Thr Met Pro
 50 55 60
 Thr His Pro Leu Tyr Pro Leu Leu Arg Leu Ala Leu Asp Phe Arg Lys
 65 70 75 80
 Thr Leu Arg Lys Lys His Arg Lys
 85

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Met Glu Asp Phe Phe Ala Trp Cys Arg Arg Gln Ser Val Leu Ser Gly
 1 5 10 15
 Ser Lys Leu Gly Arg Ala Ile Glu Tyr Ser Leu Lys Tyr Glu Glu Thr
 20 25 30

Phe Lys Thr Ile Leu Lys Asp Gly His Leu Val Leu Ser Asn Asn Leu
 35 40 45
 Ala Glu Arg Ala Ile Lys Ser Leu Val Met Gly Arg Ser Lys Arg Val
 50 55 60
 Gln Trp Thr Leu Leu Ala
 65 70

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Met Thr Lys Gln Gly Ser Trp Lys Leu Ile Leu Glu Asp Glu Ser Ala
 1 5 10 15
 Gly Arg Glu Leu Phe Pro Ile Leu Thr Gln Gly Xaa Tyr Ile Ala Thr
 20 25 30
 Phe Asp Gln Gln Ala Pro Xaa Ile Asp Glu Ile Phe Lys Leu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Met Thr Thr Asn Xaa Asp Asn Asp Thr Ser Glu Arg Ser Asp Cys Tyr
 1 5 10 15
 Arg Lys Arg Thr Ala Gly Glu Thr Pro Met Asn Asp Leu Thr Ser His
 20 25 30
 Thr His Gly Gly Asn Tyr Thr Ile Ala Arg Tyr Gln Glu Lys Phe
 35 40 45

Trp Asn Lys Gln Leu
50

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

Met Ala Gln His Ala Ala Val Glu Ala Leu Thr Ala Gly Lys Asn Asp
 1             5             10             15
Ala Glu Pro Met Lys Lys Glu Tyr Ile Gln Arg Arg Asp Tyr Ile Ile
      20             25             30
Glu Lys Met Thr Ala Leu Gly Phe Glu Ile Ile Lys Pro Asp Gly Ala
      35             40             45
Phe Tyr Ile Phe Ala Lys Ile Pro Ala Gly Tyr Asn Gln Asp Ser Phe
      50             55             60
Ala Phe Leu Lys Asp Phe Ala Gln Lys Lys Ala Val Ala Phe Ile Pro
      65             70             75             80
Gly Ala Ala Phe Gly Arg Tyr Gly Glu Gly Tyr Val Arg Leu Ser Tyr
      85             90             95
Ala Ala Ser Met Glu Thr Ile Lys Glu Ala Met Lys Arg Leu Glu Glu
      100             105             110
Tyr Met Arg Glu Ala
      115

```

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

```

Met Asn Ile Thr Asn Leu Phe Ser Ile Lys Thr Gly Cys Asp Glu Thr
 1             5             10             15
Asp Arg Gln Leu Gln Lys Leu Phe Phe Gln Leu Asp Leu Gln Leu Gly
          20             25             30
Glu Leu Thr Asp Gln Leu Arg Lys Leu Asp Ser Asn Phe Val Pro Arg
          35             40             45
Ser Gln Phe Val Asp Thr Leu Asp Leu Asn Asp Val Glu Tyr Lys Glu
          50             55             60
Ile Leu Asn Tyr Phe Ile Phe His Arg Asn Asp Ser Glu Glu Ser Leu
65             70             75             80
Val Glu Trp Leu Tyr Asp Trp Ile Ser Thr Asn Arg Tyr Glu Leu Pro
          85             90             95

```

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

```

Met Leu Gln Trp Ile Asp Arg Thr Phe Gln Asp Tyr Leu Glu Leu Glu
 1             5             10             15
His Leu Val Leu Thr Thr Trp Ser Gly Asn Leu Gly Met Met Lys Leu
          20             25             30
Ala Glu Lys Leu Xaa Met Lys Lys Xaa Ala His Ile Xaa Lys Val Arg
          35             40             45
Tyr Tyr Gln Gly Lys Tyr Phe Asp Ser Ile Lys Tyr Gly Ile Leu Arg
          50             55             60
Xaa Asp Trp Glu Lys Ile Asn Asp Gly Tyr Tyr Gln Ile Tyr Xaa Asn
65             70             75             80
Ser

```

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

```

Met Ile Val Glu Glu Val Arg Asp Arg Tyr Val Gly Lys Val Asp Ala
 1             5             10             15
Val Phe His Asn Gly Asp Ser Glu Leu Arg Pro Asp Ser Pro Leu Trp
          20             25             30
Glu Gly Ile Arg Val Val Lys Gly Asn Met Asp Phe Tyr Ala Gly Tyr
      35             40             45
Pro Glu Arg Leu Val Thr Glu Leu Gly Ser Thr Lys Ile Ile Gln Thr
      50             55             60
His Gly His Leu Phe Asp Ile Asn Phe Asn Phe Gln Lys Leu Asp Tyr
      65             70             75             80
Trp Ala Gln Glu Glu Glu Ala Ala Ile Cys Leu Tyr Gly His Leu His
          85             90             95
Val Pro Ser Ala Trp Leu Glu Gly Lys Ile Leu Phe Leu Asn Pro Gly
          100             105             110
Ser Ile Ser Gln Pro Arg Gly Thr Ile Arg Glu Cys Leu Tyr Ala Arg
          115             120             125
Val Glu Ile Asp Asp Ser Tyr Phe Lys Val Asp Phe Leu Thr Arg Asp
          130             135             140
His Glu Val Tyr Pro Gly Cys Pro Arg Ser Leu Ala Asp Asp Ala Lys
          145             150             155             160
Glu Leu Arg Leu Ser Val Gly Ala Glu Asn Phe
          165             170

```

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

```

Met Asn Leu His Gln Pro Leu His Val Leu Pro Gly Val Gly Pro Lys
 1             5             10             15

```

```

Ser Ala Glu Lys Tyr Ala Lys Leu Gly Ile Glu Asn Leu Gln Asp Leu
      20                      25                      30
Leu Leu Tyr Phe Pro Phe Arg Tyr Glu Asp Phe Lys Thr Lys Gln Val
      35                      40                      45
Leu Glu Leu Glu Asp Gly Glu Lys Ala Val Leu Ser Gly Gln Val Val
      50                      55                      60
Thr Pro Ala Ser Val Gln Tyr Tyr Gly Phe Gln Ala Ala Asn Pro Pro
      65                      70                      75                      80
Ala Phe Leu Val Leu Gln Ala Arg Glu Glu Gly Ser Phe Phe Phe Gly
      85                      90                      95
Gly

```

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

```

Met Gln Leu Leu Ser Glu Asn Met Leu Lys Thr Ile Gln Ser Leu Ser
  1                      5                      10                      15
Val Trp Gln Ile Tyr Leu Leu Gly Phe Glu Arg Ile Leu Ala Leu Gly
      20                      25                      30
Phe Gln Leu Leu Leu Thr Val Trp Val Tyr Gln Ala Val Arg Gln Lys
      35                      40                      45
Lys Trp Ile Tyr Leu Leu Ala Tyr Gly Leu His Ala Phe Phe Asp
      50                      55                      60
Leu Ala Pro Ser Leu Phe Gln Val Gly Trp Leu Thr Asn Pro Val Leu
      65                      70                      75                      80
Val Glu Val Ile Leu Ala Leu Glu Leu Val Leu Val Ala Tyr Gly Thr
      85                      90                      95
Lys Glu Ile Phe Cys Lys Lys Ser
      100

```

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

```

Met Thr Lys Ser Met Thr Pro Asp Arg Glu Val Ile Thr Phe Ile Pro
 1           5           10           15
Glu Lys Phe Ile Val Asp Gly Phe Gln Gly Ile Arg Asp Pro Arg Gly
          20           25           30
Met Met Gly Val Arg Leu Glu Met Arg Gly Leu Leu Tyr Thr Gly Pro
          35           40           45
Arg Thr Ile Leu His Asn Leu Arg Lys Thr Val Glu Arg Ala Gly Val
          50           55           60
Gln Val Glu Asn Val Ile Ile Ser Pro Leu Ala Met Val Gln Ser Val
          65           70           75           80
Leu Asn Glu Gly Glu Arg Glu Phe Gly Ala Thr Val Ile Asp Met Gly
          85           90           95
Ala Gly Gln Thr Thr Val Ala Thr Ile Arg Asn Gln Glu Leu Gln Phe
          100          105          110
Thr His Ile Leu Gln Glu Val Glu Ile Met
          115          120

```

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

```

Met Leu Asn Ser Ile Val Thr Ile Ile Cys Ile Ala Leu Ile Ala Phe
 1           5           10           15
Ile Leu Phe Trp Phe Phe Lys Lys Pro Glu Lys Ser Gly Gln Lys Ala
          20           25           30
Gln Gln Lys Asn Gly Tyr Gln Glu Ile Arg Val Glu Val Met Gly Gly
          35           40           45

```

```

Tyr Thr Pro Glu Leu Ile Val Leu Lys Lys Ser Val Pro Ala Arg Ile
  50                      55                      60
Val Phe Asp Arg Lys Asp Pro Ser Pro Cys Leu Asp Gln Ile Val Phe
  65                      70                      75                      80
Pro Asp Phe Gly Val His Ala Asn Leu Pro Met Gly Glu Glu Tyr Val
                      85                      90                      95
Val Glu Ile Thr Pro Glu Gln Ala Gly Glu Phe Gly Phe Ala Cys Gly
                      100                      105                      110
Met Asn Met Met His Gly Lys Met Ile Val Glu
                      115                      120

```

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```

Met Lys Ile Val Ser Gly Ile Tyr Gly Gly Arg Pro Leu Lys Thr Leu
  1                      5                      10                      15
Glu Gly Lys Thr Thr Arg Pro Thr Ser Asp Lys Val Arg Gly Ala Ile
                      20                      25                      30
Phe Asn Met Ile Gly Pro Tyr Phe Glu Val Gly Xaa Val Leu Asp Leu
                      35                      40                      45
Tyr Ala Gly Ser Gly Gly Leu Ser Ile Glu Ala Val Ser Arg Gly Met
                      50                      55                      60
Ser Ser Ala Val Leu Val Glu Arg Asp Arg Lys Ala Gln Thr Ile Val
                      65                      70                      75                      80
Ala Glu Asn Ile Gln Met Thr Lys Glu Val Gly Lys Phe Gln Leu Leu
                      85                      90                      95
Gln Asn Gly Cys Arg Lys Gly Ile Gly Thr Gly Xaa Leu Gly Asn Leu
                      100                      105                      110
Thr Ser Phe Ser
                      115

```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```

Met Xaa Thr Asn Phe Thr Asp Gln Val Asp Thr Met Ile Tyr Val Asp
 1             5             10             15
Lys Glu Glu Lys Glu Thr Ile Lys Ala Ala Leu Val Glu Phe Phe Asn
      20             25             30
Gly Lys Val Thr Leu Thr Asp Gln Gly Leu Arg Glu Val Glu Val Pro
      35             40             45
Val Asn Leu Val
      50

```

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```

Met Ile Gly Val Ala Leu Glu Glu Ser Pro Thr Leu Lys Ile His His
 1             5             10             15
Leu Thr His Asp Ile Thr Pro Tyr Asn Ile Phe Glu Gly Ser Tyr Arg
      20             25             30
Leu Phe Gln Thr Val Asp Tyr Trp Pro Glu Gly Thr Thr Phe Val Ser
      35             40             45
Val Val Asp Pro Gly Val Gly Ser Lys Arg Lys Ser Val Val Ala Lys
      50             55             60
Thr Ala Gln Lys Ser Ile His Cys His Ala Arg
      65             70             75

```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```

Met Glu Leu Arg Arg Pro Arg Leu Ala Asp Lys Lys Ala Val Leu Asp
 1             5             10             15
Met Met Thr Glu Phe Glu Lys Ser Gln Ser Ala His Asp Gly Gly Phe
          20             25             30
Trp Asp Thr Glu Asn Phe Val Tyr Glu Glu Trp Leu Glu Ser Asn Gln
          35             40             45
Glu Gln Glu Met Gly Ile Asn Leu Pro Glu Gly Trp Val Pro Ala Ile
          50             55             60
Gln Leu Val Ala Phe Ser Glu Lys Gly Gln Ala Val Gly Phe Leu Asn
          65             70             75             80
Leu Arg Leu Arg Leu Ser Asn Phe Leu Leu Glu Glu Gly Gly His Ile
          85             90             95
Gly Tyr Ser Ile Arg Pro Ser Glu Arg Gly Lys Gly Tyr Ala Lys Glu
          100            105            110
Leu Ser Val Arg Ala Cys Lys Leu Leu Arg Lys Arg Thr Ser Arg Lys
          115            120            125
Leu Trp
          130
  
```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```

Met Thr Phe Ile Arg Gly Pro Ile Ile Ser Thr Val Gly Glu Gly Val
 1             5             10             15
Xaa Ile Leu Ala Thr Val Asn Xaa Gln Phe Val Xaa Xaa Gln Xaa Xaa
          20             25             30
  
```

Asn Met Leu Val Ser Pro Phe His Pro Glu Leu Thr Asp Xaa Xaa Arg
 35 40 45
 Leu Xaa Gln Tyr Phe Ile Ser Met Cys Lys Glu Lys Ser Xaa Asp
 50 55 60

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Met Lys Gly Asp Val Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys
 1 5 10 15
 Asn Asn Pro Ser Ala Gln Xaa Val Leu Leu Asn Met Thr Ile Gln Lys
 20 25 30
 Val Phe Glu Lys Thr Ile Trp Leu Arg Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Met Asp Lys Ala Leu Ala Asp Leu Lys Thr Ser Gly His Leu Pro Ile
 1 5 10 15
 Pro Arg His Leu Arg Asp Gly His Tyr Xaa Gly Ser Lys Glu Leu Gly
 20 25 30
 Asn Ala Gln Asp Tyr Leu Tyr Pro His Asn Tyr Pro Xaa Asn Trp Val
 35 40 45
 Lys Gln Asp Tyr Leu Pro Gln Lys Ile Arg Asn His His Tyr Phe Gln
 50 55 60

1757020
Ala Glu Tyr Thr Gly Lys Tyr Glu Arg Ala Leu Ala Gln Arg Lys Glu
65 70 75 80
Ala Ile Asp His Leu Arg Lys Ile
85

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Val | Phe | Thr | Gly | Ser | Thr | Val | Glu | Glu | Ala | Ile | Gln | Lys | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Lys | Glu | Leu | Asp | Ile | Pro | Arg | Met | Lys | Ala | His | Ile | Lys | Val | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Arg | Glu | Lys | Lys | Gly | Phe | Leu | Gly | Leu | Phe | Gly | Lys | Lys | Pro | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gln | Val | Asp | Ile | Glu | Ala | Ile | Ser | Glu | Thr | Thr | Val | Val | Lys | Ala | Asn |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gln | Gln | Val | Val | Lys | Gly | Val | Pro | Lys | Lys | Ile | Asn | Asp | Leu | Asn | Glu |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Pro | Val | Lys | Thr | Val | Ser | Val | Arg | Asn | Arg | | | | | | |
| | | | 85 | | | | | | 90 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

Met Thr Lys Arg Cys Ser Trp Val Lys Met Thr Asn Pro Leu Tyr Ile
1 5 10 15

Ala Tyr His Asp Glu Glu Trp Gly Gln Pro Leu His Asp Asp Gln Ala
 20 25 30
 Leu Phe Glu Leu Leu Cys Met Glu Thr Tyr Gln Ala Gly Leu Ser Trp
 35 40 45
 Glu Thr Val Leu Asn Lys Arg Gln Ala Phe Arg Glu Ala Phe Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Met Phe Val Gly Gln Glu Trp Thr Asn Gln Thr Phe Val Asp Leu Leu
 1 5 10 15
 Gly Asn His Gln Gly Gln Val Thr Ile Asp Glu Glu Gly Tyr Gly Gln
 20 25 30
 Phe Pro Val Ser Ala Arg Ser Val Ser Val Trp Ala Val Asn Thr Ile
 35 40 45

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met Ala Gln Val Asp Ile Ile His Gly Ile Gly Thr Gly Val Ile Arg
 1 5 10 15
 Glu Gly Val Thr Lys Tyr Leu Gln Arg Asn Lys His Val Lys Ser Phe
 20 25 30
 Gly Tyr Ala Pro Gln Asn Ala Gly Gly Ser Gly Ala Thr Ile Val Thr
 35 40 45

Phe Lys Gly

50

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

```

Met Asn Leu Leu Glu Glu Ala Thr Lys Gly Lys Val Ile Phe Glu Gly
 1             5             10             15
Val Asp Ile Thr Asp Lys Lys Asn Asp Leu Phe Pro Met Arg Glu Lys
             20             25             30
Met Gly Met Val Phe Gln Gln Phe Asn Xaa Phe Leu Ile
             35             40             45

```

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

```

Met Gln Ile Asp Leu Ala Asn Leu Leu Pro Asp Leu Pro Gly Asn Leu
 1             5             10             15
Ser Gly Ile Asn Pro Asn Arg Tyr Val Phe Tyr Gln Asp Val Leu Cys
             20             25             30
Pro Ile Leu Asp Arg His Met Thr Pro Glu Gln Asp Lys Pro His Phe
             35             40             45
Ala Gln Ala Ala Gly Thr Ile Ala Asp Ile Lys Glu Lys Ala Gly Asn
             50             55             60
Tyr Ala Tyr Leu Phe Glu Thr Gln Ala Gln Leu Asn Ala Ile Leu Ser
             65             70             75             80

```

Ser Lys Val Asp Val Gly Arg Arg Ile Arg His Ala Tyr Gln Ala Asp
 85 90 95
 Asp Lys Glu Ser Leu Gln Gln Ile Ala Arg Gln Glu Leu Pro Glu Leu
 100 105 110
 Arg Ser Gln Ile Glu Asp Phe His Ala Leu Phe Ser His His Trp Leu
 115 120 125
 Lys

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Met Arg Gln Gly Ile Asp Ser Leu Ala Tyr Val Val Lys Thr His Phe
 1 5 10 15
 Glu Leu Asp Pro Phe Ser Gly Gln Ala Phe Leu Phe Cys Gly Gly Arg
 20 25 30
 Lys Asp Arg Phe Lys Ala Leu Tyr Trp Asp Gly Gln Gly Phe Trp Leu
 35 40 45
 Leu Tyr Lys Arg Phe Glu Asn Gly Lys Leu Thr
 50 55

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

Met Asn Ala Phe Leu Glu Glu Leu Ser Gln Ala Tyr Pro Asp Asp Tyr
 1 5 10 15

```

Phe Leu Leu Val Met Asp Asn Ala Ile Trp His Lys Ser Ser Val Leu
      20                      25                      30
Lys Ile Pro Thr Asn Ile Gly Phe Ala Phe Ile Pro Pro Tyr Thr Pro
      35                      40                      45
Glu Met Asn Pro Ile Glu Gln Val Trp Lys Glu Ile Arg Lys Arg Gly
      50                      55                      60
Phe Lys Asn Lys Ala Phe Arg Ile Leu Glu Asp Val Met Asn Gln Leu
      65                      70                      75                      80
Gln Asp Val Ile Gln Gly Leu Glu Lys Glu Val Ile Lys Ser Ile Val
      85                      90                      95
Asn Arg Arg Trp Thr Arg Met Leu Phe Glu Ser Arg
      100                      105

```

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

```

Met Thr Val Glu Glu Glu Lys Val Phe Leu Ala Arg His Leu Lys Ala
  1                      5                      10                      15
Thr Glu Ala Gly Glu Phe Val Thr Ile Asp Ala Leu Phe Gln Ala Tyr
      20                      25                      30
Lys Lys Glu Leu Gly Arg Ser Tyr Thr Arg Asp Ala Phe Tyr Gln Leu
      35                      40                      45
Leu Lys Arg His Gly Trp Arg Asn Ile Met Pro Arg Pro Glu His Pro
      50                      55                      60
Lys Lys Ala Asp Ala Gln Thr Ile Val Ala Ser Lys Asn Lys Ile Ser
      65                      70                      75                      80
Ile Gln Glu Asp Lys Lys Ala Ile
      85

```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

```

Met Leu Ser Leu Val Val Leu Ile Thr Gln Tyr Ala Thr His Gly Glu
 1             5             10             15
Leu Phe Glu Asn Tyr Ile Ser Lys Glu Asn Asp Asn Val Ile Lys Glu
             20             25             30
Tyr Gln Asn Thr Thr Gly Phe Ser Thr Pro Tyr Thr Leu Asp Gly Ser
             35             40             45
Val Leu Ile Val His Pro Asp Leu Thr Lys Gly Met Asn Ile Glu Gly
             50             55             60
Tyr Ser Asp Leu Leu Lys Pro Glu Leu Lys Gly Lys Ile Ala Thr Ala
             65             70             75             80
Asp Pro Ala Asn Ser Ser Ser Ala Phe Ala Gln Leu Thr Asn Met Leu
             85             90             95
Gln Ala Gln Gly Gly Tyr Lys Asp Asp Leu Ala Trp Ser Val Leu Ser
             100            105            110
Thr Ile Phe Ser Thr Leu Ile Asp Gly Ile Val Lys
             115            120

```

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

```

Met Leu Ala Arg Lys Asp Arg Phe Tyr Tyr Ile Asp Lys Ala Thr Gly
 1             5             10             15
Lys Ala Leu Gly Ile Phe Leu Ser Cys Val Leu Thr Ser Asn Gly Val
             20             25             30
Ile Glu Val Gly Ala Val Thr Phe Ser Pro Lys Leu Arg Gly Thr Arg
             35             40             45

```

Ile Gly Thr Glu Ala Gln Tyr Leu Leu Ala Arg Tyr Val Phe Glu Glu
 50 55 60
 Leu Asn Tyr Arg Arg Tyr Glu Trp Lys Cys Asp Ala Leu Asn Leu Pro
 65 70 75 80
 Ser Arg Arg Ala Ala Glu Arg Leu Gly Phe Ile Tyr Glu Gly Thr Phe
 85 90 95
 Arg Gln Ala Val Val Tyr Lys Gly Arg Thr Arg Asp Met Asp Trp Leu
 100 105 110
 Ser Met Ile Asp Lys Asp Trp Pro Lys Val Lys Asp Arg Leu Glu Thr
 115 120 125
 Trp Leu Arg Pro Glu Asn Phe Asp Lys Asn Gly Gln Gln Tyr Lys Ser
 130 135 140
 Leu Arg Glu Leu
 145

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Met Met Thr Ser Asp Phe Phe Glu Val Trp Phe Gln Lys Phe Leu Leu
 1 5 10 15
 Pro Thr Leu Thr Thr Pro Ser Val Ile Ile Val Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

```

Met Val Ser Thr Lys Thr Gln Ile Ala Gly Phe Glu Phe Asp Asn Cys
 1             5             10             15
Leu Met Asn Ala Ala Gly Val Ala Cys Met Thr Ile Glu Glu Leu Glu
      20             25             30
Glu Val Lys Asn Ser Ala Ala Gly Thr Phe Val Thr Lys Thr Ala Thr
      35             40             45
Leu Asp Phe Arg Gln Gly Asn Pro Glu Pro Arg Tyr Gln Asp Val Pro
      50             55             60
Leu Gly Ser Ile Asn Ser Met Gly Leu Pro Asn Asn Gly Leu Asp Tyr
65             70             75             80
Tyr Leu Asp Tyr Leu Leu Asp Leu Gln Glu Lys Glu Ser Asn Arg Thr
      85             90             95
Phe Phe Leu Ser Leu Val Gly Met Ser Pro Glu Lys Pro Ile Leu Phe
      100             105             110

```

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

```

Met Thr Tyr Leu Met Phe Ser Gly Leu Asp Glu Asn Phe Tyr His Phe
 1             5             10             15
Pro Trp Glu Val Phe Ala Gly Phe Gly Ile Ile Phe Leu Ala Cys Pro
      20             25             30
Glu Lys Val
      35

```

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

```

Met Phe Thr Gly Trp Phe Ala Gln Thr Phe Leu His Gln Phe Ile Arg
 1             5             10             15
Gly Ala Trp Gly Leu Gly Phe Met Ile Phe Ile Ala Phe Pro Met Gly
             20             25             30
Lys Glu Leu Leu Glu Gly Glu Tyr His Glu His Asp
 35             40

```

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

```

Met Gln Glu Lys Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Thr
 1             5             10             15
His Thr Val Ile Glu Leu Ile Gln Ala Gly His Gln Val Val Val Val
             20             25             30
Asp Asn Leu Val Asn Ser Asn Xaa Lys Ser Leu Glu Val Val Glu Arg
 35             40             45
Ile Thr Gly Val Glu Ile Pro Phe Tyr Glu Ala Asp Ile Xaa Asp Thr
 50             55             60
Asp Thr Leu Arg Asp Ile Phe Lys Gln Glu Glu Leu Thr Gly Val Ile
 65             70             75             80
His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Thr Arg Ile Pro Leu
             85             90             95
Ala Tyr Tyr Asp Asn Asn Ile Ala Gly Thr Val Ser Leu Leu Lys Ala
             100             105             110
Met Glu Glu Asn Asn Cys Lys Asn Ile Ile Phe Ser Ser Xaa Ala Thr
             115             120             125
Val Tyr Gly Asp Pro Tyr Thr Val Pro Ile Leu Glu Val Ser His Phe
 130             135             140
Gln
145

```

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

```

Met Val Lys Glu Lys Val Thr Leu Thr Pro Leu Ala Ser Gly Tyr Gln
 1             5             10             15
Ile Gly Glu Glu Glu Phe Glu Gln Val Ile Leu Ala Xaa Gly Ala Trp
          20             25             30
Leu Gly Asp Met Leu Glu Pro Leu Gly Tyr Glu Val Asp Val Arg Pro
          35             40             45
Gln Lys Gly Gln Leu Arg Asp Tyr Gln Leu Val Gln Asp Met Glu Ala
          50             55             60
Tyr Pro Val Val Met Pro Glu Gly Glu Trp Asp Leu Ile Pro Phe Ala
65             70             75             80
Gly Gly Lys Leu Ser Leu Gly Ala Thr His Glu Asn Asp Met Gly Phe
          85             90             95
Asp Leu Thr Val Asp Glu Thr Leu Leu Gln Gln Met Glu Glu Ala Thr
          100            105            110
Leu Thr His Tyr Leu Ile Leu Ala Glu Ala Thr Ser Lys Ser Glu Arg
          115            120            125
Val Gly Ile Arg Ala Tyr Thr Ser Asp Phe Ser Pro Phe Phe Gly Gln
          130            135            140
Val Pro Asp Leu Thr Gly Val Tyr Ala Ala Ser Gly Leu Gly Ser Ser
          145            150            155            160
Gly Leu Thr Thr Gly Pro Ile Ile Gly Tyr His Leu Ala Gln Leu Ile
          165            170            175
Gln Asp Lys Glu Leu Thr Leu Asp Pro Glu Asn Tyr Pro Ile Glu Asn
          180            185            190
Tyr Val Lys Arg Val Lys Ser Glu
          195            200

```

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

```

Met Glu His Ile Ile Tyr Gln Phe Glu Glu Asp Leu Ala Ile Leu Thr
 1             5             10             15
Leu Asn Arg Pro Glu Val Ala Asn Gly Phe His Ile Pro Met Cys Glu
          20             25             30
Glu Ile Leu Glu Ala Leu Thr Leu Ala Glu Glu Asn Pro Ala Val His
      35             40             45
Phe Ile Leu Ile Asn Ala Asn Gly Lys Val Phe Ser Val Gly Gly Asp
      50             55             60
Leu Val Glu Met Lys Arg Ala Val Asp Glu Asp Asp Ile Pro Ser Leu
65             70             75             80
Thr Lys Ile Ala Glu Leu Val Asn Thr Ile Ser Tyr Lys Ile Lys Gln
          85             90             95
Ile Ala Lys Pro Val Phe Asn Gly Ser
          100             105

```

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

```

Met Gln Pro Glu Val Ile Trp Leu Gln Lys Ile Ala Lys Pro Ser Gln
 1             5             10             15
Met Lys Val Leu Asn Thr Thr Asp Arg Val Gln Ala Ile Lys Asp Asp
          20             25             30
Val Asp Ile Ile Gln Asn Ser Leu Gln Ile Ile Asn Gln Gln Lys Glu
      35             40             45
Leu Ile Lys Glu Tyr Gln Glu Asp Leu Thr Tyr Lys Phe Lys Val Leu
      50             55             60
Glu Lys Asp Ile Gln Thr Arg Thr Ser Cys Asp Lys Arg Asn Ala Gly
65             70             75             80
Asn

```

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

```

Met Gly Ser Asn Ser Leu Thr Leu Leu Lys Ile Gln Ala Thr Ile
 1             5             10             15
Pro Arg Asn Ile Tyr Asp Asn Leu Gln Ala Gly Ser Lys Val Thr Leu
      20             25             30
Asp Arg Ala Tyr Gly His Met Ile Ile Glu Glu Gly Arg Glu Asn Gln
      35             40             45
Val Trp Ile Ala Gly Gly Ile Gly Ile Thr Pro Phe Ile Ser Tyr Ile
      50             55             60
Arg Glu His Pro Ile Leu Asp Lys Gln Val His Phe Tyr Tyr Ser Phe
65             70             75             80
Arg Gly Asp Glu Asn Ala Val Tyr Leu Asp Leu Leu Arg Asn Tyr Ala
      85             90             95
Gln Lys Asn Pro Asn Phe Glu Leu His Leu Ile Asp Ser Thr Lys Asp
      100            105            110
Gly Tyr Leu Asn Phe Glu Gln Lys Lys Cys Pro Asn Met Gln Pro Ser
      115            120            125
Ile Cys Val Val Leu Phe Leu
      130            135

```

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

```

Met Phe Phe Val Leu Ala Tyr Ala Lys Ala Val Ala Gly Arg Asn Ile
 1           5           10           15
Lys Leu His Pro Ile Gln Arg Gln Gly Ala Gly Tyr His Ser Val Asn
 20           25           30
Lys Asp Val Asp Phe Ala Ser Ala Thr Ala Leu Arg Gln His Gln Lys
 35           40           45
Asp Gln Asp Phe Leu Glu Arg Phe Met Pro Ser Val Ala Leu Phe Glu
 50           55           60
Gln Ala Ser Lys Val Ile Trp Glu Asp Tyr Phe Pro Leu Leu Arg Tyr
 65           70           75           80
Gln Ile Leu Ser Asn Pro Asp Leu Thr Thr Ile Tyr Gln Val Asn Gln
 85           90           95
Glu Met Ala Val Arg Ile Lys Glu Ala Ile Lys Thr Ala Gln Ser Val
 100          105          110
Glu Glu Leu Val Glu Leu Val Thr Thr Lys Arg Tyr Thr Lys Ala Arg
 115          120          125
Val Arg Arg Leu Leu Thr Tyr Ile Leu Met Gln Ala Arg Glu Ser Asp
 130          135          140
Leu Pro Glu Ala Ile His Val Leu Gly Phe Thr Glu Lys Gly Arg Gln
 145          150          155          160
His Leu Lys Ser Leu Lys Gly Gln Val Asn Leu Val Ser Arg Ile Gly
 165          170          175
Lys Glu Pro Trp Asp Ala Met Thr Gln Lys Val Asp Gln Ile Tyr Gln
 180          185          190
Leu Gly Lys Pro Ser Ile Ala Glu Gln Asn Phe Gly Arg Val Pro Ile
 195          200          205
Arg Ile Glu Thr Asn
 210

```

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

```

Met Leu Gly Ser Met Phe Val Gly Leu Leu Val Gly Phe Leu Ala Gly
 1           5           10           15

```

Ala Met Thr Asn Arg Gly Glu Arg Met Gly Cys Phe Gly Lys Met Phe
 20 25 30
 Leu Gly Trp Ile Gly Ala Phe Leu Gly His Leu Leu Phe Gly Thr Trp
 35 40 45
 Gly Pro Val Leu Ser Gly Thr Ala Ile Ile Pro Ala Val Leu Gly Ala
 50 55 60
 Met Ile Val Leu Ala Ile Phe Trp Arg Arg Gly Ser
 65 70 75

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Met Arg Ser Ser Pro Ser Arg Glu Ile Gln Pro Arg Ser Trp Gly Ile
 1 5 10 15
 Thr Thr Val Tyr Val Thr His Asp Gln Glu Gly Ala Met Ala Ile Ser
 20 25 30
 Asp Gln Ile Ala Cys Tyr Glu Arg Trp Gly Asp Pro Thr Asn Arg Pro
 35 40 45
 Thr Lys Arg Thr Val Ser
 50

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:
 - 5 (a) a polynucleotide having at least a 70% identity to a polynucleotide encoding a polypeptide comprising an amino acid sequence of selected from the group consisting of SEQ ID NO:224 through 477,
 - (b) a polynucleotide which is complementary to the polynucleotide of (a);
 - (c) a polynucleotide having at least a 70% identity to a polynucleotide encoding the
10 same mature polypeptide expressed by the a gene comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1 through 223 contained in the DNA of the deposited clone; and
 - (d) a polynucleotide comprising at least 15 sequential bases of the polynucleotide of (a), (b) or (c).
- 15 2. The polynucleotide of Claim 1 wherein the polynucleotide is DNA.
3. The polynucleotide of Claim 1 wherein the polynucleotide is RNA.
4. The polynucleotide of Claim 2 comprising the nucleic acid sequence set forth in SEQ ID NO:1.
5. The polynucleotide of Claim 2 comprising a nucleotide sequence selected from
20 the group consisting of SEQ ID NO:1 through 223.
6. The polynucleotide of Claim 2 which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:224 through 477.
7. A vector comprising the polynucleotide of Claim 1.
8. A host cell comprising the vector of Claim 7.
- 25 9. A process for producing a polypeptide comprising: expressing from the host cell of Claim 8 a polypeptide encoded by said DNA.
10. A process for producing a novel polypeptide or fragment comprising culturing a host of claim 8 under conditions sufficient for the production of said polypeptide or fragment.
- 30 11. A polypeptide comprising an amino acid sequence which is at least 70% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:224 through 477.
12. A polypeptide comprising an amino acid selected from the group consisting of SEQ ID NO:224 through 477.

13. An antibody against the polypeptide of claim 11.
14. An antagonist which inhibits the activity or expression of the polypeptide of claim 11.
15. A method for the treatment of an individual in need of a Streptococcal polypeptide comprising: administering to the individual a therapeutically effective amount of the polypeptide of claim 11.
16. A method for the treatment of an individual having need to inhibit a bacterial polypeptide comprising: administering to the individual a therapeutically effective amount of the antagonist of Claim 14.
17. A process for diagnosing a disease related to expression or activity of the polypeptide of claim 11 in an individual comprising:
 - (a) determining a nucleic acid sequence encoding said polypeptide, and/or
 - (b) analyzing for the presence or amount of said polypeptide in a sample derived from the individual.
18. A method for identifying compounds which interact with and inhibit or activate an activity of the polypeptide of claim 11 comprising:
 - contacting a composition comprising the polypeptide with the compound to be screened under conditions to permit interaction between the compound and the polypeptide to assess the interaction of a compound, such interaction being associated with a second component capable of providing a detectable signal in response to the interaction of the polypeptide with the compound;
 - and determining whether the compound interacts with and activates or inhibits an activity of the polypeptide by detecting the presence or absence of a signal generated from the interaction of the compound with the polypeptide.
19. A method for inducing an immunological response in a mammal which comprises inoculating the mammal with Streptococcal polypeptide of claim 11, or a fragment or variant thereof, adequate to produce antibody and/or T cell immune response to protect said animal from disease.
20. A method of inducing immunological response in a mammal which comprises delivering a nucleic acid vector to direct expression of Streptococcal polypeptide of claim 11, or fragment or a variant thereof, for expressing said Streptococcal polypeptide, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibody and/or T cell immune response to protect said animal from disease.

21. An isolated Streptococcal polypeptide having one of the amino acid sequences of SEQ ID NO:224 through SEQ ID NO:234.
22. An isolated nucleic acid encoding one of the amino acid sequences of Claim 21 and nucleic acid sequences capable of hybridizing therewith under stringent conditions.
23. Recombinant vectors comprising the nucleic acid sequences of Claim 22 and host cells transformed or transfected therewith.
24. A method of identifying an antimicrobial compound comprising contacting candidate compounds with a polypeptide of Claim 21 and selecting those compounds capable of inhibiting the bioactivity of said polypeptide.
25. Antimicrobial compounds identified by the method of Claim 24.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/05306

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : 536/23.7; 435/6, 69.1, 252.3, 320.1; 530/324, 350; 514/12

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.7; 435/6, 69.1, 252.3, 320.1; 530/324, 350; 514/12

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---------------------|--|--|
| X, P --- Y, P | WO 96/10647 A1 (FUSO PHARMACEUTICAL INDUSTRIES, LTD.) 11 April 1996, claim 2, pages 22-24. | 1, 2, 7, 8, and 22 ----- 3, 6, 9-12, 15, 17, 21, and 23-25 |
| Y | WATSON, J. D. et al. Recombinant DNA, Second Edition. New York: Scientific American Books, W.H. Freeman and Company, 1992, pages 73 and 74, see entire document. | 1-3, 6-12, 15, 17, and 21-23 |
| Y | KENNEL, D. E. Principles and Practices of Nucleic Acid Hybridization. Progress in Nucleic Acid Research Molecular Biology. 1971, Vol. 11, pages 259-301, see especially pages 259-262. | 1-3, 6-12, 15, 17, and 21-23 |

☐ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

* Special categories of cited documents:

A document defining the general state of the art which is not considered to be of particular relevance

B earlier document published on or after the international filing date

L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

Z

document member of the same patent family

Date of the actual completion of the international search

10 JULY 1997

Date of mailing of the international search report

06 AUG 1997

 Name and mailing address of the ISA/US
 Commissioner of Patents and Trademarks
 Box PCT
 Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

JAMES MARTINELL

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05306

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-3, 6-12, 15, 17, and 21-23 (SEQ ID NOs 224-233).

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05306

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING (Continued):

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I. Claims 1-12, 15, 17, and 21-23, drawn to nucleic acids and polypeptides of specific sequence, vectors containing nucleic acids, methods of producing polypeptides, and methods of treatment using polypeptides.

Group II. Claims 13 and 19, drawn to antibodies against any of no fewer than 254 specific sequence polypeptides.

Group III. Claims 14 and 16, drawn to antagonists of undisclosed composition of the activity of no fewer than 254 specific sequence polypeptides.

Group IV. Claims 18 and 24, drawn to methods for screening for compounds that interact with no fewer than 254 specific sequence polypeptides.

Group V. Claim 20, drawn to a method of inducing an immunological response using a nucleic acid.

Group VI. Claim 25, drawn to compounds of undisclosed composition.

The inventions listed as Groups I-VI do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons. The nucleic acids, proteins, and methods of Group I are materially different from the antibodies of Group II, the compounds of Group III, and the compounds of Group VI and are not required to produce either the antibodies of Group II, which antibodies may be made with antigens other than those embraced by Group I. Additionally, the methods of Group I are not needed to produce the compounds of either one of Groups III or VI. The compositions and methods of Group I are not needed for the methods of either one of Groups IV or V. The antibodies of Group II are not needed for the methods of Groups IV or V and are materially different from the compounds of Groups III and VI. The antagonists of Group III are materially different from the compounds of Group VI because the antagonists and compounds have differing sites of action and/or binding. Neither are the compounds of either one of Groups III or VI needed to practice the methods of either one of Groups IV or V. The methods of Groups IV and V may be practiced independently of one another.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows. Each of the 234 SEQ ID NOs listed is a separate species because there is no relationship between the species.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons. There is no relationship among the species.

For any Group applicant elects, a total of 10 (TEN) specified sequences will be searched and no more than 4 (FOUR) specified sequences will be searched for each additional fee paid.

The claims are deemed to correspond to the species listed above in the following manner: SEQ ID NOs 224-233 correspond to claims 1-3, 6-12, 15, 17, and 21-23.

A. CLASSIFICATION OF SUBJECT MATTER: IPC (6):

C12N 15/31, 15/11, 15/00; C12P 21/02; A61K 38/16, 39/09; C07K 14/195, 14/315

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

MFSRCH OF: A-GENESEQ26, A-ISSUED, HIV-AA2, PIR50, SUTWW-PROT34, EMBL-NEW11, GENBANK97, GENBANK-NEW11, U-EMBL48_97, HIV-NA8, N-GENESEQ26, N-ISSUED, EST-STS, EST-STS-TWO, EST-STS-

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05306

THREE. SEQ ID NOs 224-233.